

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 10:11:26 ; Search time 1905 Seconds
(without alignments)
10136.138 Million cell updates/sec

Title: US-10-045-116-1

Perfect score: 472

Sequence: 1 AGCCACACACGAGCCT.....ACGTTCTGCAACTCAAGCA 472

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	471	99.8	3500	6	AX705342	AX705342 Sequence
2	471	99.8	11288	6	AR134885	AR134885 Sequence
3	471	99.8	11288	6	AR182304	AR182304 Sequence
4	471	99.8	11288	6	AX269130	AX269130 Sequence
5	471	99.8	11288	9	HSCRCANTA	HSCRCANTA
6	471	99.8	15056	6	AR266427	AR266427 Sequence
7	471	99.8	15056	6	AX259954	AX259954 Sequence
8	471	99.8	15056	6	AX262359	AX262359 Sequence
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14	271.8	57.6	3500	6	AX705405	AX705405 Sequence
15	264.8	56.1	645	9	HSCGM2PRO	HSCGM2PRO
c 16	263.2	55.8	39753	9	AC005797	AC005797 Homo sapi
c 17	263	55.7	3500	6	AX705384	AX705384 Sequence
c 18	256.6	54.4	3500	6	AX705406	AX705406 Sequence
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22	156.6	33.2	2073	9	HUMCEANCA	HUMCEANCA
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c 24	128.8	27.3	2450	9	HSACGM1	HSACGM1
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ALIGNMENTS

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX705342
Sequence 11 from Patent WO03014388.
AX705342
AX705342.1 GI:29562007

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Distler, J., Model, F. and Taubert, H.

Method and nucleic acids for the analysis of colon cancer

JOURNAL

Pred. No. is the number of results predicted by chance to have a

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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 6.3e-141; Indels 0; Gaps 0;
Matches 471; Conservative 0; Mismatches 0;
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LOCUS ARL134885 11288 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6194211.
ACCESSION ARL134885
VERSION ARL134885.1 GI:14123790
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11288)
AUTHORS Richards,C.Ann. and Huber,B.
TITLE Transcriptional regulatory sequence of carcinoembryonic antigen for expression targeting
JOURNAL Patent: US 6194211-A 1 27-FEB-2001;
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DEFINITION Sequence 4 from patent US 6337209.
ACCESSION ARL182304
VERSION ARL182304.1 GI:20225220
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11288)
AUTHORS Huber,B. and Richards,C.A.
TITLE Molecular constructs containing a carcinoembryonic antigen regulatory sequence
JOURNAL Patent: US 6337209-A 4 08-JAN-2002;
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Epigenomics AG (DE)
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QY 421 GCAGACAGACAGTCACAGCAGCTTGACAAAAGCTTCCTGGAACTCAAGC 471
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RESULT 2
LOCUS ARL134885 11288 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6194211.
ACCESSION ARL134885
VERSION ARL134885.1 GI:14123790
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11288)
AUTHORS Richards,C.Ann. and Huber,B.
TITLE Transcriptional regulatory sequence of carcinoembryonic antigen for expression targeting
JOURNAL Patent: US 6194211-A 1 27-FEB-2001;
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DEFINITION Sequence 1 from Patent WO0174861.
ACCESSION AX269130
VERSION AX269130.1 GI:16542049
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Vile,R.G., Harrington,K., Murphy,S. and Bateman,A.
TITLE Compositions and methods for tissue specific gene regulation
therapy
JOURNAL Patent: WO 0174861-A 1 11-OCT-2001;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
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DEFINITION H.sapiens carcinoembryonic antigen gene.
ACCESSION Z21818
VERSION Z21818.1 GI:437783
KEYWORDS carcinoembryonic antigen.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Schrewe,H., Thompson,J., Bona,M., Hefta,L.J., Maruya,A., Hassauer,M., Shively,J.E., von Kleist,S. and Zimmermann,W.
TITLE Cloning of the complete gene for carcinoembryonic antigen: analysis of its promoter indicates a region conveying cell type-specific expression
JOURNAL Mol. Cell. Biol. 10 (6), 2738-2748 (1990)
MEDLINE 90258861
PUBMED 2342461
REMARK (sites)
REFERENCE 2 (bases 1 to 11288)
AUTHORS Richards,C.A., Wolberg,A.S. and Huber,B.E.
TITLE The transcriptional control region of the human carcinoembryonic antigen gene: DNA sequence and homology studies
JOURNAL DNA Seq. 4 (3), 185-196 (1993)
MEDLINE 94214170
PUBMED 8161821
REFERENCE 3 (bases 1 to 11288)
AUTHORS Richards,C.A., Austin,E.A. and Huber,B.E.
TITLE Transcriptional regulatory sequences of carcinoembryonic antigen: identification and use with cytosine deaminase for tumor-specific gene therapy
JOURNAL Hum. Gene Ther. 6 (7), 881-893 (1995)
MEDLINE 96097131
PUBMED 7378407
REFERENCE 4 (bases 1 to 11288)
AUTHORS Richards,C.A.
TITLE Direct Submission
JOURNAL Submitted (24-FEB-1993) Richards C. A., Burroughs Wellcome Co., Cell Biology, 3030 Cornwallis Rd, Research Triangle Park, North Carolina, USA, 27709
COMMENT Overlapping sequence: U17131.
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Best Local Similarity	100.0%; Pred. No. 7.2e-141;
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DEFINITION	Sequence 10 from patent US 6495130.
ACCESSION	AR266427
VERSION	AR266427.1 GI:29695383
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SOURCE	Unknown.
ORGANISM	Unknown.
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LOCUS AX262359 15056 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 14 from Patent WO01/73093.
ACCESSION AX262359
VERSION AX262359.1 GI:16511287
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Yu,D.C., Li,Y. and Henderson,D.R.
TITLE Cell-specific adenovirus vectors comprising an internal ribosome
entry site
JOURNAL Patent: WO 01/73093-A 14 04-OCT-2001;
Calydon, Inc. (US)
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DEFINITION Homo sapiens chromosome 19 clone LLNLR-269B9, complete sequence.
ACCESSION AC008999
VERSION AC008999.7 GI:15281189
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 39707)
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Direct Submission
Unpublished
2 (bases 1 to 39707)
DOE Joint Genome Institute.
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 39707)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (03-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 39707)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (26-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
5 (bases 1 to 39707)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (23-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Aug 23, 2001 this sequence version replaced gi:11079409.
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www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
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DEFINITION	Sequence 1 from Patent WO9404156.	
ACCESSION	A37261	
VERSION	A37261.1 GI:2294358	
KEYWORDS	unidentified	
SOURCE	unclassified	
ORGANISM	unclassified	
REFERENCE	1 (bases 1 to 3281)	
AUTHORS	Vile,R.G. and Hart,I.R.	
TITLE	TUMOUR THERAPY	
JOURNAL	Patent: WO 9404196-A 1 03-MAR-1994;	
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QY	1	AGCCACACCCAGTGAGCCCTTTTCTAGCCCCCAGAGCCACCTCTGTCACTTCTCTGTG	60	
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LOCUS	HUMCEA01	3281 bp	DNA linear	PRI 06-MAR-1995			
DEFINITION	Human carcinoembryonic antigen (CEA) gene, complete cds.						
ACCESSION	M59255 M31966						
VERSION	M59255.1 GI:180200						
KEYWORDS	carcinoembryonic antigen.						
SEGMENT	1 of 10						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	Schrewe,H., Thompson,J., Bona,M., Hefta,L.J., Maruyama,A., Hassauer,M., Shively,J.E., von Kleist,S. and Zimmermann,W. Cloning of the complete gene for carcinoembryonic antigen: analysis of its promoter indicates a region conveying cell type-specific expression						
TITLE							
JOURNAL	Mol. Cell. Biol.	10 (6),	2738-2748	(1990)			
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Best Local Similarity 98.9%; Pred. No. 2e-128;
Matches 467; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

QY	1	AGCCACACCCAGTGAGCCCTTTTCTAGCCCCAGAGCCACCTCTGTCACTTCTCTGTG	60
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QY	121	TTTCTCTGTACAAAGGAAATTAATCCCTTGGTGTGACAGACCCCAAGGACAGAACAG	180
Db	1380	TTTCTCTGTACAAAGGAAATTAATCCCTTGGTGTGACAGACCCCAAGGACAGAACAG	1439
QY	181	CAGAGGTCAGCACTGGG-AAAGACAGTTGTCTCCAGGGGATGGGGTTCATCAACT	239
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QY	360	ACGTGATGCTGSAAGTACTCTCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAGAC	419
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QY	420	AGCACCACGACAGTCACAGCAGCCTTGACAAAAGTTCTCGAAGCTCAAGC	471
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LOCUS	AX705383	3500 bp	DNA	linear	PAT 04-APR-2003
DEFINITION	Sequence 52 from Patent WO03014388.				
ACCESSION	AX705383				
VERSION	AX705383.1	GI:29562048			
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SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Distler, J., Modei, F. and Taubert, H.				
TITLE	Method and nucleic acids for the analysis of colon cancer				
JOURNAL	Patent: WO 03014388-A 52 20-FEB-2003;				
FEATURES	Epigenomics AG (DE)				
source	Location/Qualifiers				
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ORIGIN					

Query Match

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DEFINITION Sequence 74 from Patent WO03014388.
ACCESSION AX705405
VERSION AX705405.1 GI:29562070
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Distler,J., Model,F. and Taubert,H.
TITLE Method and nucleic acids for the analysis of colon cancer
JOURNAL Patent: WO 03014388-A 74 20-FEB-2003;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers
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DEFINITION H.sapiens carcinoembryonic antigen family member 2, CGM2, promoter
region.
ACCESSION X98312
VERSION X98312.1 GI:1524061
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CGM2 gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Seitz,M., Chastre,E., Ditter,M., Aldrian,C.,
Gespach,C. and Zimmermann,W.
TITLE Down-regulation of carcinoembryonic antigen family member 2
expression is an early event in colorectal tumorigenesis
JOURNAL Cancer Res. 57 (9), 1776-1784 (1997)
MEDLINE 97280695
PubMed 9135022
REFERENCE 2 (bases 1 to 645)
AUTHORS Zimmermann,W.
TITLE Direct Submision
JOURNAL Submitted (24-MAY-1996) W. Zimmermann, Albert-Ludwigs-University,
Institute of Immunobiology, Stefan-Meier-Strasse 8, D-79104
Freiburg, FRG
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GenCore version 5.1.6
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2	471	99.8	11288	16 AAQ90511	CEA clone HindIII-
3	471	99.8	11288	23 AAS14778	Human carcinoembry
4	471	99.8	15056	19 AAV52967	Carcinoembryonic a
5	471	99.8	15056	21 AAA46851	Nucleotide sequenc
6	471	99.8	15056	21 AAZ99933	DNA sequence of co
7	471	99.8	15056	22 AAH43620	CEA-TRE. Homo sap
8	471	99.8	15056	23 AAF87238	CEA-TRE fusion pro

9	471	99.8	15056	24 ABK99582	Prostate-specific
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11	225	47.7	271	20 AAZ09584	Carcinoembryonic a
12	120.8	25.6	39801	14 ABK83462	Human cDNA differe
13	94	19.9	3774	16 AAQ73990	CEA Clone HindIII
14	85.8	18.2	39801	24 ABK83462	Human cDNA differe
15	75	15.9	2974	24 ABN95819	Gene #2317 used to
16	75	15.9	2974	24 ABL64746	Lung cancer relate
17	75	15.9	2974	25 ABX76144	Lung cancer-associ
18	75	15.9	2974	25 ABQ83855	Human CEA encoding
19	75	15.9	2975	24 ABQ82535	Human CEA nucleoti
20	75	15.9	2975	24 ABQ82535	Human colon cancer
21	69.4	14.7	653	22 ABQ60586	Human foetal liver
22	60.6	12.8	474	22 ABAS3345	Human brain expres
23	60.6	12.8	474	22 ABA28046	Human bone marrow
24	60.6	12.8	474	22 AAK07563	Probe #6360 for ge
25	60.6	12.8	474	22 AAI16427	Probe #7832 used t
26	60.6	12.8	474	22 AAI16427	Human liver single
27	60.6	12.8	474	22 AAI39146	Human genome-deriv
28	60.6	12.8	474	23 ABS33113	Human lung tumour
29	60.6	12.8	474	24 ABS08194	Human lung tumour-
30	59	12.5	1298	21 AAC77896	cDNA encoding huma
31	57.6	12.2	387	20 AAZ08319	Human colon tumour
32	57.6	12.2	387	21 AAC79171	Human secreted pro
33	57.6	12.2	387	23 AAD23246	Human secreted pro
34	57.2	12.1	460	21 AAA77889	Human secreted pro
35	57.2	12.1	460	22 AAI28627	Human secreted pro
36	57.2	12.1	460	22 AAI28627	Human secreted pro
37	56.4	11.9	319	21 AAC10830	CDNA encoding colo
38	55.4	11.7	294	24 ABK44760	Human secreted pro
39	54.8	11.6	306	21 AAC10828	Human secreted pro
40	54.8	11.6	327	21 AAC10827	Human secreted pro
41	54.8	11.6	414	21 AAC10829	Human secreted pro
42	54.6	11.6	504	21 AAC10831	Human secreted pro
43	54.2	11.5	502	21 AAC04586	Human secreted pro
44	54.2	11.5	2115	21 AAC10826	Human secreted pro
45	54	11.4	2220	17 AAT33302	Carcinoembryonic a

ALIGNMENTS

RESULT 1
AAV52944
ID AAV52944 standard; DNA; 472 Bp.
XX AC AAV52944;
XX DT 21-DEC-1998 (first entry)
XX DE CEA transcriptional regulatory element (CEA-TRE).
XX DE Carcinoembryonic antigen; transcriptional regulatory element;
XX KW CEA-TRE; human; promoter; enhancer; adenovirus; vector; cancer;
XX KW gene therapy; ds.
XX OS Homo sapiens.
XX PN WC9839467-A2.
XX PD 11-SEP-1998.
XX PF 03-MAR-1998; 98WO-US04133.
XX PR 02-MAR-1998; 98US-0039763.
XX PR 03-MAR-1997; 97US-0039763.
XX (CALY-) CALYDON INC.
XX PI Henerson DR, Lamparski HG, Schuur ER;
XX DR WPI; 1998-495862/42.

PT New adenovirus vectors, particularly for cancer therapy - comprising
PT adenovirus gene under transcriptional control of carcinoembryonic
XX antigen transcriptional regulatory element
PS Claim 13; Page 62-63; 95pp; English.

XX This 472 nucleotide fragment comprises nucleotides -402 to +69
CC of the human carcinoembryonic antigen transcriptional regulatory
CC element (CEA-TRE). It was isolated from human genomic DNA by PCR
CC (see AAV52945-46). The CEA-TRE is capable of expressing gene
CC expression specific to cells capable of expressing CEA or capable
CC of CRE-TRE-mediated transcription. A claimed replication-competent
CC adenovirus (Ad) vector comprises an Ad gene under transcriptional
CC control of a CEA-TRE. Also claimed are: (1) a host cell transformed
CC with a Ad vector as above; (2) a method of making a masked Ad, and
CC (3) an Ad complexed with a masking agent. By providing for
CC transcriptional initiating regulation dependent upon CEA
CC expression, virus replication can be restricted to target cells
CC which allow a CEA-TRE to function, particularly carcinoma cells
CC expressing CEA. The vectors can be used to detect and monitor
CC samples for the presence of cells that allow a CEA-TRE to function,
CC and to selectively kill such cells, especially malignant cells.
CC Preferred vectors contain a CEA-TRE comprising nucleotides 313-472
CC or 104-472 of the 472 nucleotide fragment, especially comprising an
CC enhancer and/or a promoter of the CEA gene.

XX Sequence 472 BP; 142 A; 125 C; 134 G; 71 T; 0 other;

Query Match 100.0%; Score 472; DB 19; Length 472;
Best Local Similarity 100.0%; Pred. No. i.le-127;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACACCCAGTGGAGCCCTTTCTAGCCCCCAGAGCCACTCTGTCACTTCTCTGTG 60
DB 1 AGCCACACCCAGTGGAGCCCTTTCTAGCCCCCAGAGCCACTCTGTCACTTCTCTGTG 60
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCCGGACCTGCTGGG 120
DB 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCCGGACCTGCTGGG 120
QY 121 TTTCTCTGTCAAGAGAAATATATCCCTCTGGTGTGACAGACCCCAAGGACAGACACAG 180
DB 121 TTTCTCTGTCAAGAGAAATATATCCCTCTGGTGTGACAGACCCCAAGGACAGACACAG 180
QY 181 CAGAGGTGACAGCTGGGAGACAGAGTGTCTCTCCAGGGATGGGGTCCATCCACCTT 240
DB 181 CAGAGGTGACAGCTGGGAGACAGAGTGTCTCTCCAGGGATGGGGTCCATCCACCTT 240
QY 241 GCCGAAAAGATTGTCTGAGGAAGTAAATAGAGGAAAGAGAGGAGGACAAAAGA 300
DB 241 GCCGAAAAGATTGTCTGAGGAAGTAAATAGAGGAAAGAGAGGAGGACAAAAGA 300
QY 301 GGCAGAAATGAGAGGGGAGGACAGAGACACCTGTAATAAGACACACCCATGACCA 360
DB 301 GGCAGAAATGAGAGGGGAGGACAGAGGACACCTGTAATAAGACACACCCATGACCA 360
QY 361 CGTATGCTGAGAGTACTCTCTGAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
DB 361 CGTATGCTGAGAGTACTCTCTGAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
QY 421 GCAGACCAGACAGTCAAGAGCCCTTGACAAACCTTCTGGAACCTCAAGCA 472
DB 421 GCAGACCAGACAGTCAAGAGCCCTTGACAAACCTTCTGGAACCTCAAGCA 472

RESULT 2
AAQ90512
ID AAQ90512 standard; DNA; 11288 BP.

XX
AC AAQ90512;
XX
DT 25-MAR-2003 (updated)
DT 01-NOV-1995 (first entry)

XX CEA clone HindIII-Sau3A fragment.
DE
XX Carcinoembryonic antigen; CEA; transcription regulatory sequence;
KW TRS; gene targeting; cancer; metastasis; gene therapy;
KW cytosine deaminase; ss.

XX Homo sapiens.
XX WO9514100-A2.
XX 26-MAY-1995.
XX 18-NOV-1994; 94WO-GB02546.
XX 19-NOV-1993; 93US-0154712.
XX (WELL) WELLCOME FOUND LTD.
XX Huber B, Richards CA;
XX WPI; 1995-200389/26.
XX New carcinoembryonic antigen transcriptional regulatory sequence DNA -
PT used partic. for expressing heterologous enzymes for pro-drugs in the
PT treatment of cancers

XX Disclosure; Page 31-37; 64pp; English.

XX CEA genomic clone lambdaCEA1 was isolated from human chromosome 19
CC genomic library LL19N101 (ATCC 57766). An HindIII/Sau3A fragment
CC of the clone extended from -10.7 to +0.6 kb relative to the start
CC site of CEA mRNA. TRS regions of CEA are used to target e.g.
CC cytosine deaminase to cancer cells for prodrug activation.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 11288 BP; 2940 A; 3063 C; 2953 G; 2332 T; 0 other;

Query Match 99.8%; Score 471; DB 16; Length 11288;
Best Local Similarity 100.0%; Pred. No. 8.2e-127;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACACCCAGTGGAGCCCTTTCTAGCCCCCAGAGCCACTCTGTCACTTCTCTGTG 60
DB 10294 AGCCACACCCAGTGGAGCCCTTTCTAGCCCCCAGAGCCACTCTGTCACTTCTCTGTG 10353
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCCGGACCTGCTGGG 120
DB 10354 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCCGGACCTGCTGGG 10413
QY 121 TTTCTCTGTCAAGAGAAATATATCCCTCTGGTGTGACAGACCCCAAGGACAGACACAG 180
DB 10414 TTTCTCTGTCAAGAGAAATATATCCCTCTGGTGTGACAGACCCCAAGGACAGACAG 10473
QY 181 CAGAGGTGACAGCTGGGAGAGAGTGTCTCTCCAGGGATGGGGTCCATCCACCTT 240
DB 10474 CAGAGGTGACAGCTGGGAGAGAGTGTCTCTCCAGGGATGGGGTCCATCCACCTT 10533
QY 241 GCCGAAAAGATTGTCTGAGGAAGTAAATAGAGGAAAGAGAGGAGGACAAAAGA 300
DB 10534 GCCGAAAAGATTGTCTGAGGAAGTAAATAGAGGAAAGAGAGGAGGACAAAAGA 10593
QY 301 GGCAGAAATGAGAGGGGAGGAGGAGACACCTGTAATAAGACACACCCATGACCA 360
DB 10594 GGCAGAAATGAGAGGGGAGGAGGAGACACCTGTAATAAGACACACCCATGACCA 10653
QY 361 CGTATGCTGAGAGTACTCTCTGAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
DB 10654 CGTATGCTGAGAGTACTCTCTGAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 10713
QY 421 GCAGACCAGACAGTCAAGAGCCCTTGACAAACCTTCTGGAACCTCAAGC 471
DB 10714 GCAGACCAGACAGTCAAGAGCCCTTGACAAACCTTCTGGAACCTCAAGC 10764

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RESULT 3
AAS14778
ID AAS14778 standard; DNA; 11288 BP.
XX
AC AAS14778;
XX
DT 27-FEB-2002 (first entry)
XX
DE Human carcinoembryonic antigen (CEA) genomic DNA.
XX
KW Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine;
KW syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour;
KW recombinase; tumour-specific promoter; hypoxic response element; HRE; ds;
KW tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer;
KW cytostatic; gene therapy; human.
XX
OS Homo sapiens.
XX
FH Key
FT Location/Qualifiers
FT CDS
FT /*tag= a
FT /product= "Human carcinoembryonic antigen"
XX
PN WO200174861-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10250.
XX
PR 31-MAR-2000; 2000US-193977P.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI Vile RG, Harrington K, Murphy S, Bateman A;
XX
DR WPI; 2001-656985/75.
XX
XX
XX Recombinant nucleic acid vector for reducing tumour size, has expression
XX cassette comprises a promoter linked to nucleic acid sequence encoding
XX a syncytium-inducing polypeptide and flanked on either side by
XX recombinase
XX
XX Disclosure; Fig 3; 84pp; English.
XX
XX The invention relates to a recombinant nucleic acid vector comprising a
XX first expression cassette, comprising a first promoter operably linked to
XX a nucleic acid sequence encoding a syncytium-inducing polypeptide (such
XX as a fusogenic membrane glycoprotein) and flanked on either side by a
XX sequence recognised by a recombinase, and/or a second expression cassette
XX comprising a tumour-specific promoter operably linked to a nucleic acid
XX sequence encoding a recombinase. The nucleic acid of the first expression
XX cassette may be linked to a hypoxic response element (HRE), the second
XX expression cassette may contain a promoter linked to a nucleic acid
XX encoding a cytokine, and a third cassette may contain a tumour specific
XX promoter linked to the nucleic acid encoding the recombinase. The tumour
XX specific promoter is, for example, a carcinoembryonic antigen (CEA)
XX promoter or a tyrosinase promoter and the recombinase is, for example,
XX Cre recombinase or FLP recombinase. The invention is useful for reducing
XX tumour size by administering the compositions as retroviral vectors, or
XX in a cell containing the vector, to an individual in need of treatment
XX for a disease caused by malignant cells. This sequence represents genomic
XX DNA encoding the human carcinoembryonic antigen (CEA).
XX
XX Sequence 11288 BP; 2944 A; 3060 C; 2955 G; 2329 T; 0 other;
XX
XX Query Match 99.8%; Score 471; DB 23; Length 11288;
XX Best Local Similarity 100.0%; Pred. No. 8.2e-127;
XX Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ACCCACCCAGTGGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
XX |||||||
XX

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Db 10294 AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTCACTTCCGTG 10353
QY 61 GGCAATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGGACCTGCTGGG 120
Db 10354 GGCAATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGGACCTGCTGGG 10413
QY 121 TTTCTCTGTCACAAAAGGAAATAATCCCTTGGTGTGACAGACCCCAAGGACACACAG 180
Db 10414 TTTCTCTGTCACAAAAGGAAATAATCCCTTGGTGTGACAGACCCCAAGGACACACAG 10473
QY 181 CAGAGTCTAGCAGTCTGGGGAAGACAGGTTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 10474 CAGAGTCTAGCAGTCTGGGGAAGACAGGTTCTCTCCAGGGGATGGGGTCCATCCACCTT 10533
QY 241 GCCGAAAGATTTGTTCTGAGGAACTGAAATAAGAGGAAAAAAGAGGAGGACAAAAGA 300
Db 10534 GCCGAAAGATTTGTTCTGAGGAACTGAAATAAGAGGAAAAAAGAGGAGGACAAAAGA 10593
QY 301 GGCAGAAATGAGAGGGGGGACAGAGGACACCTGTAATAAGACCCACACCCATGACCCA 360
Db 10594 GGCAGAAATGAGAGGGGGGACAGAGGACACCTGTAATAAGACCCACACCCATGACCCA 10653
QY 361 CGTGATGCTGAGAAGTACTCTCTGAGGAACTGAGGAGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 10654 CGTGATGCTGAGAAGTACTCTCTGAGGAACTGAGGAGAGGAGGAGGAGGAGGAGGAGGAG 10713
QY 421 GCAGACCAGACAGTCACAGCAGCCCTTGACAAAACCTTCTCGAACTCAAGC 471
Db 10714 GCAGACCAGACAGTCACAGCAGCCCTTGACAAAACCTTCTCGAACTCAAGC 10764

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RESULT 4
AAS2967
ID AAV52967 standard; DNA; 15056 BP.
XX
AC AAV52967;
XX
DT 21-DEC-1998 (first entry)
XX
DE Carcinoembryonic antigen gene 5' flanking region.
XX
KW Carcinoembryonic antigen; transcriptional regulatory element;
KW CEA-TRE; human; promoter; enhancer; adenovirus; vector; cancer;
KW gene therapy; ds.
XX
OS Homo sapiens.
XX
FH Key
FT Location/Qualifiers
FT misc_feature
FT /*tag= a
FT /label= CEA-TRE
FT /note= "nucleotides -402 to +69 (Claim 13)"
XX
PN WO9839467-A2.
XX
PD 11-SEP-1998.
XX
PF 03-MAR-1998; 98WO-US04133.
XX
PR 02-MAR-1998; 98US-0039763.
XX
PR 03-MAR-1997; 97US-0039763.
XX
XX (CALY-) CALYDON INC.
XX
PI Benerson DR, Lamparski HG, Schuur ER;
XX
DR WPI; 1998-495862/42.
XX
XX New adenovirus vectors, particularly for cancer therapy - comprising
XX adenovirus gene under transcriptional control of carcinoembryonic
XX antigen transcriptional regulatory element
XX
XX Disclosure; Fig 2A-K; 95pp; English.
XX

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XX This nucleotide sequence comprises the 5' flanking region of the
CC human carcinoembryonic antigen (CEA) gene to nucleotide +537
CC relative to the transcriptional start. A 472 bp fragment (see
CC AAV52944) of this 5' flanking region (nucleotides -402 to +69)
CC comprises the CEA transcriptional regulatory element (CEA-TRE) that
CC is capable of mediating gene expression specific to cells capable
CC of expressing CEA or capable of CRE-TRE-mediated transcription. A
CC claimed replication-competent adenovirus (Ad) vector comprises an
CC Ad gene under transcriptional control of a CEA-TRE. By providing
CC for transcriptional initiating regulation dependent upon CEA
CC expression, virus replication can be restricted to target cells
CC which allow a CEA-TRE to function, particularly carcinoma cells
CC expressing CEA. The vectors can be used to detect and monitor
CC samples for the presence of cells that allow a CEA-TRE to function,
CC and to selectively kill such cells, especially malignant cells.
XX
SQ Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 other;

Query Match 99.8%; Score 471; DB 19; Length 15056;
Best Local Similarity 100.0%; Pred. No. 9.2e-127;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACACCCAGTGAGCCCTTTCTAGCCCCCAGAGCCACTCTGCACCTTCCTGTG 60
Db |||||||
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGGACCCCTGCTGG 120
Db |||||||
QY 14122 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGGACCCCTGCTGG 14181
Db |||||||
QY 121 TTCTCTGTGCACAAAGGAAATATATCCCTGTTGACAGACCCCAAGGAGACAGACAG 180
Db |||||||
QY 14182 TTCTCTGTGCACAAAGGAAATATATCCCTGTTGACAGACCCCAAGGAGACAGACAG 14241
Db |||||||
QY 181 CAGAGGTACAGCTGGGAGAGCATGGTTCCTCCAGGGATGGGGTCCATCCACTT 240
Db |||||||
QY 14242 CAGAGGTACAGCTGGGAGAGCATGGTTCCTCCAGGGATGGGGTCCATCCACTT 14301
Db |||||||
QY 241 GCCGAAAGATTTGCTGAGGAACCTGAAATAGAGGGAAGGAAAGAGAGGAGGACAAAGA 300
Db |||||||
QY 14302 GCCGAAAGATTTGCTGAGGAACCTGAAATAGAGGGAAGGAAAGAGAGGAGGACAAAGA 14361
Db |||||||
QY 301 GGCAGAAATGAGAGGGAGGGGACAGAGGACACCTGAAATAGAGGAGGAGGAGGAGGAGGAG 360
Db |||||||
QY 14362 GGCAGAAATGAGAGGGAGGGGACAGAGGACACCTGAAATAGAGGAGGAGGAGGAGGAGGAG 14421
Db |||||||
QY 361 CGTATGCTGAGAGAGTACTCTGCTAGGAGAGACTCAGGGCAGAGGAGGAGGAGGAGGAGGAG 420
Db |||||||
QY 14422 CGTATGCTGAGAGAGTACTCTGCTAGGAGAGACTCAGGGCAGAGGAGGAGGAGGAGGAGGAG 14481
Db |||||||
QY 421 GCAGACCAGACAGTCACAGCAGCCTTGACAAACCTGCTTGAACCTCAAGC 471
Db |||||||
QY 14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAACCTGCTTGAACCTCAAGC 14532
Db |||||||

RESULT 5
ID AAA46851
XX AAA46851 standard; DNA; 15056 BP.
AC AAA46851;
XX
DT 03-OCT-2000 (first entry)
XX
DE Nucleotide sequence of a CEA-TRE.
XX
KW Adenoviral vector; adenoviral gene; E3 sequence; cancer;
KW target cell-specific transcriptional regulatory element; TRE;
KW selective cytotoxicity; cell growth; tumour growth; ss.
XX
OS Homo sapiens.
XX
PN W0200039319-A2.

XX 06-JUL-2000.
XX 30-DEC-1999; 99WO-US31249.
XX 30-DEC-1998; 98US-0114262.
XX 29-DEC-1999; 99US-0474699.
XX (CALY-) CALYDON INC.
XX Henderson DR, Yu D;
XX WPI; 2000-452409/39.
XX
XX New adenoviral vector for selective targeting of cancer cells,
XX comprises an adenovirus gene under transcriptional control of a target
XX cell-specific transcriptional regulatory element and an E3 sequence -
XX Disclosure; Fig 23; 138pp; English.
XX
XX The specification describes an adenoviral vector which comprises an
XX adenoviral gene under the transcriptional control of a target
XX cell-specific transcriptional regulatory element (TRE) and an E3
XX sequence. The vectors are useful for exerting selective cytotoxicity
XX and/or suppressing cell growth (including tumour growth). This is
XX especially useful in treating cancer in which targeted cell killing is
XX desirable. This is also useful for targeted cytotoxic effects in other,
XX non-tumour cells, when selective destruction and/or suppression of these
XX cells is desirable. The vectors can also be useful for detecting the
XX presence of cells which permit function of a target cell-specific TRE in,
XX for example, an appropriate biological (such as clinical) sample. The
XX adenovirus vector(s) can optionally selectively produce one or more
XX proteins of interest in a target cell by using a heterologous, i.e.,
XX non-adenoviral, TRE. The present sequence represents a CEA-TRE, which
XX is used in the course of the invention.
XX
SQ Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 other;

Query Match 99.8%; Score 471; DB 21; Length 15056;
Best Local Similarity 100.0%; Pred. No. 9.2e-127;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACACCCAGTGAGCCCTTTTCTAGCCCCCAGAGCCACTCTGTGCTTCCTGTG 60
Db |||||||
QY 14062 AGCCACACCCAGTGAGCCCTTTTCTAGCCCCCAGAGCCACTCTGTGCTTCCTGTG 14121
Db |||||||
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGGACCCCTGCTGG 120
Db |||||||
QY 14122 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGGACCCCTGCTGG 14181
Db |||||||
QY 121 TTCTCTGTGCACAAAGGAAATATATCCCTGTTGACAGACCCCAAGGAGACAGACAG 180
Db |||||||
QY 14182 TTCTCTGTGCACAAAGGAAATATATCCCTGTTGACAGACCCCAAGGAGACAGACAG 14241
Db |||||||
QY 181 CAGAGGTACAGCTGGGAGAGCATGGTTCCTCCAGGGATGGGGTCCATCCACTT 240
Db |||||||
QY 14242 CAGAGGTACAGCTGGGAGAGCATGGTTCCTCCAGGGATGGGGTCCATCCACTT 14301
Db |||||||
QY 241 GCCGAAAGATTTGCTGAGGAACCTGAAATAGAGGGAAGGAAAGAGGAGGAGGAGGAGGAG 300
Db |||||||
QY 14302 GCCGAAAGATTTGCTGAGGAACCTGAAATAGAGGGAAGGAAAGAGGAGGAGGAGGAGGAG 14361
Db |||||||
QY 301 GGCAGAAATGAGAGGGAGGGGACAGAGGACACCTGAAATAGAGGAGGAGGAGGAGGAGGAG 360
Db |||||||
QY 14362 GGCAGAAATGAGAGGGAGGGGACAGAGGACACCTGAAATAGAGGAGGAGGAGGAGGAGGAG 14421
Db |||||||
QY 361 CGTATGCTGAGAGAGTACTCTGCTAGGAGAGACTCAGGGCAGAGGAGGAGGAGGAGGAGGAG 420
Db |||||||
QY 14422 CGTATGCTGAGAGAGTACTCTGCTAGGAGAGACTCAGGGCAGAGGAGGAGGAGGAGGAGGAG 14481
Db |||||||
QY 421 GCAGACCAGACAGTCACAGCAGCCTTGACAAACCTGCTTGAACCTCAAGC 471
Db |||||||
QY 14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAACCTGCTTGAACCTCAAGC 14532
Db |||||||

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RESULT 6
AAZ99933
ID AAZ99933 standard; DNA; 15056 BP.
XX
AC AAZ99933;
XX
DT 25-JUL-2000 (first entry)
XX
DE DNA sequence of comprising a carcinoembryonic antigen TRE.
XX
KW Carcinoembryonic antigen; adenoviral vector; adenovirus gene;
KW transcriptional regulatory element; TRE; transcriptional control;
KW adenoviral propagation; tumour; ss.
XX
OS Unidentified.
XX
XX WO200015820-A1.
XX
PD 23-MAR-2000.
XX
PF 10-SEP-1999; 99WO-US20718.
XX
PR 10-SEP-1998; 98US-0099791.
PR 09-SEP-1999; 99US-0099791.
XX
PA (CALY-) CALYDON INC.
XX
PI Yu DC, Henderson DR;
XX
DR WPI; 2000-271456/23.
XX
XX Adenovirus vectors comprising cell-status specific response elements
XX useful in gene therapy protocols for the treatment of cancers -
XX
PS Disclosure; Fig 5A-I; 79pp; English.
XX
XX The present sequence comprises a transcriptional regulatory element
XX (TRE) from a carcinoembryonic antigen gene. The TRE is used to
XX produce an adenoviral vector of the invention. The specification
XX describes an adenovirus vector which comprises an adenovirus gene
XX under transcriptional control of a cell status specific TRE. The
XX TRE is preferably one that is essential for adenoviral propagation.
XX The adenovirus vectors may be used for the treatment of a range of
XX tumours such as lung, stomach, breast, colon and rectum, and uterine
XX and cervix cancers.
XX
SQ Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 other;

Query Match          99.8%; Score 471; DB 21; Length 15056;
Best Local Similarity 100.0%; Pred. No. 9.2e-127;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACCACCCAGTCAGCTTTTCTAGCCCCCAGAGCCACCTCTGTCACTTCTCTGTG 60
Dd 14062 AGCCACCACCCAGTCAGCTTTTCTAGCCCCCAGAGCCACCTCTGTCACTTCTGTG 14121
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGACCCCTGCTGG 120
Dd 14122 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGACCCCTGCTGG 14181
QY 121 TTTCTCTGTCAAGAAATAATATCCCTGGTGTGTACAGACCCAGGACAGAACACAG 180
Dd 14182 TTTCTCTGTCAAGAAATAATATCCCTGGTGTGTACAGACCCAGGACAGAACACAG 14241
QY 181 CAGAGGTGACACTGGGGAACAGAGTTGCTTCCAGGGGATGGGGTCCATCCACCT 240
Dd 14242 CAGAGGTGACACTGGGGAACAGAGTTGCTTCCAGGGGATGGGGTCCATCCACCT 14301
QY 241 GCGGAAAGATTGTCTGAGAACTGAAATAGAGGAAAGAGAGGGGACAAAGA 300
Dd 14302 GCGGAAAGATTGTCTGAGAACTGAAATAGAGGAAAGAGAGGGGACAAAGA 14361

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QY 301 GGCAGAAATGAGAGGGGGGACAGAGGACACCTGAATAAAGAACACCCATGACCA 360
Dd 14362 GGCAGAAATGAGAGGGGGGACAGAGGACACCTGAATAAAGAACACCCATGACCA 14421
QY 361 CTTGATGCTGAGAAGTACTCTGCTAGGAGAGACTCAGGCGAGAGGAGGAGGACA 420
Dd 14422 CTTGATGCTGAGAAGTACTCTGCTAGGAGAGACTCAGGCGAGAGGAGGAGGACA 14481
QY 421 GCAGACCAGACAGTCACAGAGCCCTTGACAAAACGTTCTGGAACCTCAAGC 471
Dd 14482 GCAGACCAGACAGTCACAGAGCCCTTGACAAAACGTTCTGGAACCTCAAGC 14532

RESULT 7
AAH43620
ID AAH43620 standard; cDNA; 15056 BP.
XX
AC AAH43620;
XX
DT 07-JAN-2002 (first entry)
XX
DE CEA-TRE.
XX
XX Adenovirus; ADP; replication-competent; adenoviral vector; TRE; PCR;
KW transcriptional regulatory element; mutation; deletion; IRES; primer;
KW promoter; internal ribosome entry site; cytotoxic; cancer; bladder;
KW amplify; polymerase chain reaction; alpha-fetoprotein; AFP; EMCV;
KW encephalomyocarditis virus; vascular endothelial growth factor; VEGF;
KW immunoglobulin heavy-chain binding protein; BiP; uroplakin II; PDGF;
KW platelet derived growth factor; hypoxia responsive element; HRE;
KW prostate-specific antigen; PSA; ss.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT precursor_RNA 14466..15056
FT /*tag= a
FT /note= "transcription start site"
XX
XX WO200173093-A2.
XX
XX 04-OCT-2001.
XX
XX 21-MAR-2001; 2001WO-US09036.
XX
XX 24-MAR-2000; 2000US-192156P.
XX
XX (CALY-) CALYDON INC.
XX
XX Yu D, Li Y, Henderson DR;
XX
XX WPI; 2001-639234/73.
XX
XX Replication-competent adenoviral vector, useful e.g. for killing cancer
XX cells, contains two genes linked by internal ribosome entry site and
XX controlled by target-specific regulator -
XX
XX Example; Page 117-125; 148pp; English.
XX
XX The sequences given in AAH43607-22 represent sequences which may be used
XX in the replication-competent adenoviral vector (A) of the invention.
XX The vector contains two genes (G1, G2) that are co-transcribed as a
XX single mRNA and under control of a heterologous, target cell-specific
XX transcriptional regulatory element (TRE). G2 has a mutation in, or
XX deletion of, its endogenous promoter and is controlled from an internal
XX ribosome entry site (IRES). (A) has greater specificity for a target
XX cell than a similar vector in which IRES is operably linked to a gene
XX and which lacks an IRES. (A) are used to modify the genotype of target
XX cells, optionally in vitro with subsequent return of altered cells to
XX the host and where G2 is a cytotoxic gene, to confer selective cyto-
XX toxicity to target cells, especially for killing cancer cells. Also
XX (A) are used for diagnosis and monitoring, e.g. detection of bladder

```

CC cancer cells. The target cell-specific TRE ensures that (A) has better
CC targeting specificity, with minimal replication in non-target cells, so
CC a runaway infection is prevented but production of adenoviral proteins
CC in target cells activates and/or stimulates the immune response against
CC target cells producing such proteins. The use of an IRES (rather than
CC two identical control elements) eliminates the risk of homologous
CC recombination and may provide enough extra space for an additional
CC (therapeutic) gene.
XX
SQ Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 other;

Query Match 99.8%; Score 471; DB 22; Length 15056;
Best Local Similarity 100.0%; Pred. No. 9.2e-127;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCACCCAGTGGAGCTTTCTAGCCCGCCAGAGCCCTCTCTCACTTCCTGTTG 60
DB 14062 AGCCACCCAGTGGAGCTTTCTAGCCCGCCAGAGCCCTCTCTCACTTCCTGTTG 14121
QY 61 GGCATCATCCAGCTTCCAGAGCCCTGGAGATGGGGAGAGCCCGGACCTGCTGGG 120
DB 14122 GGCATCATCCAGCTTCCAGAGCCCTGGAGATGGGGAGAGCCCGGACCTGCTGGG 14181
QY 121 TTCTCTGTCTACAAAGAAATTAATCCCTGTGTGACAGACCCCAAGGACACACAG 180
DB 14182 TTCTCTGTCTACAAAGAAATTAATCCCTGTGTGACAGACCCCAAGGACACACAG 14241
QY 181 CAGAGTTCAGCTGGGAGAGAGCTTGTCTCCAGAGGATGGGGGTCCATCCACCTT 240
DB 14242 CAGAGTTCAGCTGGGAGAGAGCTTGTCTCCAGAGGATGGGGGTCCATCCACCTT 14301
QY 241 GCCGAAAGATTTCTGTAGGAACTGAAATAGAGGAAAGAGAGGGGACAAAAGA 300
DB 14302 GCCGAAAGATTTCTGTAGGAACTGAAATAGAGGAAAGAGAGGGGACAAAAGA 14361
QY 301 GGCAGAAATGAGAGGGGAGGAGCAGAGGACACCTGTAATAGACACACCCATGACCCA 360
DB 14362 GGCAGAAATGAGAGGGGAGGAGCAGAGGACACCTGTAATAGACACACCCATGACCCA 14421
QY 361 CGTGATGCTGAGAGTACTCTGCTAGGAGAGCTCAGGGCAGAGGAGGAGGACA 420
DB 14422 CGTGATGCTGAGAGTACTCTGCTAGGAGAGCTCAGGGCAGAGGAGGAGGACA 14481
QY 421 GCAGACAGACAGTCACAGAGCCTTGACAAAAGCTTCCTGGAACTCAAGC 471
DB 14482 GCAGACAGACAGTCACAGAGCCTTGACAAAAGCTTCCTGGAACTCAAGC 14532

RESULT 8
ID AAF87238 standard; DNA; 15056 BP.
XX AAF87238;
AC AAF87238;
XX
XX
XX 26-MAR-2002 (first entry)
XX CEA-TRE fusion protein coding sequence.
XX Tumour growth suppression; adenovirus vector; antineoplastic agent;
KW transcriptional regulatory element; TRE; radiotherapy; bladder cancer;
KW prostate cancer; liver cancer; breast cancer; colon cancer; melanoma;
KW ovarian cancer; pancreatic cancer; lung cancer; brain cancer; therapy;
KW CEA-TRE; ds.
XX
XX Homo sapiens.
OS
XX WO200172341-A2.
PN
XX
XX 04-OCT-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US09042.
PF
XX
XX 24-MAR-2000; 2000US-192015P.
PR

XX (CALY-) CALYDON INC.
PA Yu D, Chen Y, Henderson DR;
XX WPI; 2001-648426/74.
XX
XX Suppression of tumour growth, e.g. liver, bladder or breast cancer,
PT comprises using a synergistic combination of adenovirus vector and
PT antineoplastic agent or radiotherapy -
XX
XX Claim 12; Page 185-193; 248pp; English.
PS
XX This sequence represents a CEA-TRE fusion protein coding sequence
CC used in the scope of the invention. The invention relates to a method
CC for the suppression of tumour growth comprising the administration of:
CC (a) a target cell-specific adenovirus vector comprising an adenoviral
CC gene essential for replication under transcriptional control of a
CC target cell-specific transcriptional regulatory element (TRE); and
CC (b) at least one antineoplastic agent; or (c) a course of radiotherapy
CC where the amount of (a) and/or (b) or (c) is lower than that known to be
CC effective for suppressing tumour growth when administered alone.
CC The method is used for suppression of tumour growth for treatment of
CC e.g. bladder cancer, prostate cancer, liver cancer, breast cancer, colon
CC cancer, melanoma, ovarian cancer, pancreatic cancer, lung cancer or brain
CC cancer. The combinations enhance the efficacy of treatment, allowing
CC lower doses to be administered, reducing toxicity and suffering of the
CC patient.
XX
SQ Sequence 15056 BP; 3848 A; 4126 C; 4010 G; 3072 T; 0 other;

Query Match 99.8%; Score 471; DB 23; Length 15056;
Best Local Similarity 100.0%; Pred. No. 9.2e-127;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCACCCAGTGGAGCTTTCTAGCCCGCCAGAGCCCTCTCTCACTTCCTGTTG 60
DB 14062 AGCCACCCAGTGGAGCTTTCTAGCCCGCCAGAGCCCTCTCTCACTTCCTGTTG 14121
QY 61 GGCATCATCCAGCTTCCAGAGCCCTGGAGATGGGGAGAGCCCGGACCTGCTGGG 120
DB 14122 GGCATCATCCAGCTTCCAGAGCCCTGGAGATGGGGAGAGCCCGGACCTGCTGGG 14181
QY 121 TTCTCTGTCTACAAAGAAATTAATCCCTGTGTGACAGACCCCAAGGACACACAG 180
DB 14182 TTCTCTGTCTACAAAGAAATTAATCCCTGTGTGACAGACCCCAAGGACACACAG 14241
QY 181 CAGAGTTCAGCTGGGAGAGAGCTTGTCTCCAGAGGATGGGGGTCCATCCACCTT 240
DB 14242 CAGAGTTCAGCTGGGAGAGAGCTTGTCTCCAGAGGATGGGGGTCCATCCACCTT 14301
QY 241 GCCGAAAGATTTCTGTAGGAACTGAAATAGAGGAAAGAGAGGGGACAAAAGA 300
DB 14302 GCCGAAAGATTTGTCTAGGAACTGAAATAGAGGAAAGAGAGGGGACAAAAGA 14361
QY 301 GGCAGAAATGAGAGGGGAGGAGCAGAGGACACCTGTAATAGACACACCCATGACCCA 360
DB 14362 GGCAGAAATGAGAGGGGAGGAGCAGAGGACACCTGTAATAGACACACCCATGACCCA 14421
QY 361 CGTGATGCTGAGAGTACTCTGCTAGGAGAGCTCAGGGCAGAGGAGGAGGACA 420
DB 14422 CGTGATGCTGAGAGTACTCTGCTAGGAGAGCTCAGGGCAGAGGAGGAGGACA 14481
QY 421 GCAGACAGACAGTCACAGAGCCTTGACAAAAGCTTCCTGGAACTCAAGC 471
DB 14482 GCAGACAGACAGTCACAGAGCCTTGACAAAAGCTTCCTGGAACTCAAGC 14532

RESULT 9
ID ABK99582 standard; DNA; 15056 BP.
XX ABK99582;
AC ABK99582;

XX 21-OCT-2002 (first entry)
XX Prostate-specific antigen transcriptional regulatory element (TRE).
XX Adenovirus; transcriptional regulatory element; TRE; prostate; liver;
XX breast cancer; colon cancer; antitumor; gene; ds; probasin; PB; human;
XX rat; carcinoembryonic antigen; prostate-specific antigen; ADP;
XX adenovirus death protein; glandular kallikrein.
XX Unidentified.
XX US2002068049-A1.
XX 06-JUN-2002.
XX 06-DEC-2000; 2000US-0732169.
XX 10-SEP-1998; 98US-0151376.
XX (HEND/) HENDERSON D R.
XX (SCHU/) SCHUUR E R.
XX Henderson DR, Schuur ER;
XX WPI; 2002-582468/62.
XX Novel adenovirus vector comprises adenovirus gene under transcriptional
XX control of cell-type specific transcriptional response element for
XX conferring selective toxicity on target cell and for suppressing tumor
XX growth -
XX Disclosure; Fig 15; 83pp; English.
XX The invention relates to an adenovirus vector (AV) comprising an AV gene
XX under transcriptional control of a cell type-specific transcriptional
XX regulatory element (TRE) and optionally a first AV gene under control of
XX a first cell type-specific TRE and a second gene under control of a
XX second cell type-specific TRE, where the first and second cell
XX type-specific TREs are substantially identical. When the vector is
XX introduced into a cell (e.g. prostate cell, liver cell, breast cancer
XX cell or colon cancer cell) it allows the cell type-specific TRE to
XX function, resulting in cytotoxicity. The vector is useful for suppressing
XX tumour growth of a target cell. This sequence represents a polynucleotide
XX used in the scope of the invention.
XX Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 other;
XX
XX Query Match 99.8%; Score 471; DB 24; Length 15056;
XX Best Local Similarity 100.0%; Pred. No. 9,2e-127; Mismatches 0; Indels 0; Gaps 0;
XX Matches 471; Conservative 0;
XX
XX QY 1 AGCCACCACCCAGTCTTTCTAGCCCCAGAGCCACCTCTGTACCTTCCTGTGG 60
XX DB 14062 AGCCACCACCCAGTCTTTCTAGCCCCAGAGCCACCTCTGTACCTTCCTGTGG 14121
XX QY 61 GSCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGACCTGTCTGG 120
XX DB 14122 GSCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGACCTGTCTGG 14181
XX QY 121 TTCTCTGTCAAAAGGAAATAATCCCTCTGTGTGACAGACCCAGGAGACACAG 180
XX DB 14182 TTCTCTGTCAAAAGGAAATAATCCCTCTGTGTGACAGACCCAGGAGACACAG 14241
XX QY 181 CAGAGTCTGACACTGGGAGACAGGTGTCTCTCCAGGGATGGGGTCCATCCACTT 240
XX DB 14242 CAGAGTCTGACACTGGGAGACAGGTGTCTCTCCAGGGATGGGGTCCATCCACTT 14301
XX QY 241 GCCGAAAAAGATTGTCTCAGGAACCTGAAATAGAGGGAAGGAGAGGAGGACAAAAGA 300
XX DB 14302 GCCGAAAAAGATTGTCTCAGGAACCTGAAATAGAGGGAAGGAGAGGAGGACAAAAGA 14361
XX QY 301 GCGAGAAATGAGAGGGAGGGGACAGAGACACCTGTAATAAGACCACCCATGACCCA 360

DB 14362 GGCAGAAATGAGAGGGAGGAGGACAGAGACCTGTAATAAGACACACCATGACCA 14421
QY 361 CQTGATGCTGAGAAGTACTCTCTGCTAGGAAGAGACTCAGGGCAGAGGAGGAGGACA 420
DB 14422 CQTGATGCTGAGAAGTACTCTCTGCTAGGAAGAGACTCAGGGCAGAGGAGGAGGACA 14481
QY 421 CGAGACCCAGACAGTCACAGCAGCCCTTGACAAAACGTTCTTGGAACTCAAGC 471
DB 14482 CGAGACCCAGACAGTCACAGCAGCCCTTGACAAAACGTTCTTGGAACTCAAGC 14532
XX
XX RESULT 10
XX AAQ90511
XX ID AAQ90511 standard; DNA; 14556 BP.
XX AC AAQ90511;
XX 25-MAR-2003 (updated)
XX DT 01-NOV-1995 (first entry)
XX DE CEA genomic clone.
XX KW Carcinoembryonic antigen; CEA; transcription regulatory sequence;
XX TRS; gene targeting; cancer; metastasis; gene therapy;
XX KW cytosine deaminase; hybridization; probe; ss.
XX OS Homo sapiens.
XX PN W09514100-A2.
XX 26-MAY-1995.
XX 18-NOV-1994; 94WO-GB02546.
XX 19-NOV-1993; 93US-0154712.
XX (WELL) WELLCOME FOUND LTD.
XX PA Huber B, Richards CA;
XX WPI; 1995-200389/26.
XX New carcinoembryonic antigen transcriptional regulatory sequence DNA -
XX used partic. for expressing heterologous enzymes for pro-drugs in the
XX treatment of cancers
XX Disclosure; Fig. 6; 64pp; English.
XX CEA genomic clone lambdaDACEAL was isolated from human chromosome 19
XX genomic library L19NL01 (ATCC 57766). HindIII/Sau3A and HindIII
XX fragments of the clone were sequenced and combined to obtain the
XX sequence given in AAQ90511, which extends from -14.4 to +0.6 kb
XX relative to the start site of CEA mRNA.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 14556 BP; 3721 A; 3995 C; 3874 G; 2966 T; 0 other;
XX
XX Query Match 76.1%; Score 359; DB 16; Length 14556;
XX Best Local Similarity 96.9%; Pred. No. 4.3e-94;
XX Matches 443; Conservative 0; Mismatches 0; Indels 14; Gaps 7;
XX
XX QY 1 AGCCACCACCCAGTCTTTCTAGCCCCAGAGCCACCTCTGTACCTTCCTGTGG 60
XX DB 13594 AGCCACCACCCAGTCTTTCTAGCCCCAGAGCCACCTCTGTACCTTCCTGTGG 13651
XX QY 61 GSCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGACCCCTCTCTGG 120
XX DB 13652 GSCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGACCCCTCTCTGG 13709
XX QY 121 TTCTCTGTCAAAAGGAAATAATCCCTCTGTGTGACAGACCCAGGAGACACAG 180
XX DB 13710 TTCTCTGTCAAAAGGAAATAATCCCTCTGTGTGAGACCCAGGAGACACAG 13767

Qy	181	CAGAGGTGAGCACTGGGAGACAGACGTTGTCTCTCCAGGGGATGGGGTTCATCCACCTT	240
Db	13768	CAGAGGTCAGCACTGGGAGACAGAGTTGTCTCCCA--GGATGGGGTTCATCCACCTT	13825
Qy	241	GCCTAAAACGATTGTCTGAGGAACTCGAAATAGAAAGGGAATAAGAGAGGAGCAAAAAGA	300
Db	13826	GCCTAAAACGATTGTCTGAGGAACTCGAAATAGAAAGG--AATAAGAGAGGAGCAAAAAGA	13883
Qy	301	GCAGAAATGAGAGGGAGGGGACAGAGGACACTGTAATAAGACCACCCATGACCCA	360
Db	13884	GCAGAAATGAGAGGGAGGGGACAGAGGACACCTGGA--AAAGACACACCCATGACCCA	13941
Qy	361	CGTGATGTCGAGAAGTACTCTCTGCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGACA	420
Db	13942	CGTGATGTCGAGAAGTACTCTCTGCCCTAGGAGAGACA--CAGGGCAGAGGGAGGAGGACA	13999
Qy	421	GCAGACGACACAGTCACAGCAGCCTTGACAAAACGTT	457
Db	14000	GCAGACGACACAGTCACAGCAGCCTTGACAAAACGTT	14036

RESULT 11	
AAZ09584	
ID	AAZ09584 standard; DNA; 271 BP.
XX	
XX	
AC	AAZ09584;
XX	
XX	
DT	05-NOV-1999 (first entry)
XX	
XX	
DE	Carcinoembryonic antigen homologue promoter.
XX	
XX	
KW	Carcinoembryonic antigen; CEA; promoter; colon cancer; gene therapy;
KW	tumour; secretion; tumour cell; ss.
XX	
XX	
OS	Unidentified.
XX	
PN	CN1216321-A.
XX	
XX	
PD	12-MAY-1999.
XX	
XX	
FF	31-OCT-1997; 97CN-0114280.
XX	
XX	
PR	31-OCT-1997; 97CN-0114280.
XX	
XX	
PA	(SCRE-) SCI RES & TRAINING SECTION MEDICAL MATTE.
XX	
XX	
PI	Jiang Y, Wang X, Xie B;
XX	
DR	WPI: 1999-431041/37.
XX	

XX Cloning carcinoembryonic antigen promoter DNA - used for tumour gene
PT therapy
XX
XX Claim 3; Page 3; 10pp; Chinese.
PS
XX This invention describes a novel DNA sequence which is dissimilar from
CC the carcinoembryonic antigen (CEA) promoter of colon cancer. In CEA
CC secretory tumour gene therapy, the gene segment is recombined with a
CC therapeutic gene, so that killing of tumour cells may be effected
CC selectively while keeping normal cells unaffected. This sequence
CC represents promoter used to describe the method of the invention.
XX
XX Sequence 271 BP; 100 A; 57 C; 82 G; 32 T; 0 other;
SQ

Query Match	47.7%	Score 225;	DB 20;	Length 271;
Best Local Similarity	100.0%;	Pred. No. 1.1e-55;		
Matches 225;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	247	AAAGATTTCCTGAGGAACTGAAATGAAGGGGAAAAAGAGGGGACAAAGAGGCACA	306	
Db	1	AAAGATTTCCTGAGGAACTGAAATGAAGGGGAAAAAGAGGGGACAAAGAGGCACA	60	

		367	GCTCAGAAAGTACTCCTGCCCTPAGGAAGAGACTCAGGGCAGAGGGAGGAGGACAGCAGAC	426
		121	GCTCAGAAAGTACTCCTGCCCTPAGGAAGAGACTCAGGGCAGAGGGAGGAGGACAGCAGAC	180
Qy		427	CAGACACTCAGCAGACGAGCCTTGACAAAACGTTCTCTGGAACTCAAGC	471
Dd		181	CAGACAGTCACAGCAGAGCCTTGACAAAACGTTCTCTGGAACTCAAGC	225
		307	AATCAGAGGGAGGGGACAGAGGACACCTGTAATAAAGACACACCCATTACCCACGTGAT	366
		61	AATCAGAGGGAGGGGACAGAGGACACCTGTAATAAAGACACACCCATTACCCACGTGAT	120

RESULT 12	
ABR83462/C	
ID	ABR83462 standard; cDNA; 39801 BP.
XX	
AC	ABR83462;
XX	
DT	14-AUG-2002 (first entry)
XX	
XX	Human cDNA differentially expressed in granulocytic cells #33.
XX	
KW	Human; ss: granulocytic cell; DNA chip; bacterial infection;
KW	viral infection; parasitic infection; protozoal infection;
KW	fungal infection; sterile inflammatory disease; psoriasis;
KW	rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW	cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW	adult respiratory distress syndrome; inflammatory bowel disease;
KW	Crohn's disease; ulcerative colitis; periodontal disease;
KW	granulocyte activation; chronic inflammation; allergy.

XX	Homo sapiens.
XX	WO200228999-A2.
XX	11-APR-2002.
XX	03-OCT-2001; 2001WO-US30821.
XX	03-OCT-2000; 2000US-237189P.
XX	(GENE-) GENE LOGIC INC.
XX	Beazer-Bartclay Y, Weissman SM, Yamaga S, Vockley J;
XX	WPI; 2002-435328/46.
XX	Detecting granulocyte activation by detecting differential expression
XX	of genes associated with granulocyte activation, which serves as
XX	diagnostic markers that is useful for monitoring disease states and
XX	drug toxicity -
XX	Claim 1: SPO ID NO 33: 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GCA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having

SQ Sequence 2974 BP; 840 A; 847 C; 613 G; 674 T; 0 other;
 Query Match 15.9%; Score 75; DB 24; Length 2974;
 Best Local Similarity 100.0%; Pred. NO. 1.6e-11;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 397 CTCAGGGCAGAGGGAGGAGGACAGCAGACACAGTACAGTCCCTTGACAAAACGT 456
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 CTCAGGGCAGAGGGAGGAGGAGGACAGCAGACACAGTACAGTCCCTTGACAAAACGT 456
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 457 TCCTGGAACTCAAGC 471
 ||||||||||||||||
 Db 61 TCCTGGAACTCAAGC 75
 ||||||||||||||||

Search completed: September 26, 2003, 12:34:57
 Job time : 251 secs

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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 12:22:31 ; Search time 71 Seconds
(without alignments)
2934.265 Million cell updates/sec

Title: US-10-045-116-1

Perfect score: 472

Sequence: 1 AGCCACCACCCAGTGGCCG.....ACGTTCTCGAATCAAGCA 472

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	472	100.0	472	4	US-09-033-556-7
2	471	99.8	11288	3	US-08-646-301A-1
3	471	99.8	11288	4	US-08-481-968A-4
4	471	99.8	11288	4	US-08-154-712B-4
5	471	99.8	15056	4	US-09-474-699-10
6	94	19.9	3774	3	US-08-646-301A-2
7	94	19.9	3774	4	US-08-481-968A-5
8	94	19.9	3774	4	US-08-154-712B-5
9	71.2	15.1	7218	1	US-08-232-463-14
10	57.6	12.2	387	4	US-09-370-838-177
11	54	11.4	2220	1	US-08-389-459A-16
12	54	11.4	2220	3	US-08-987-867A-16
13	44.2	9.4	319	3	US-09-385-982-486
14	39.2	8.3	289	3	US-09-007-005-17
15	39.2	8.3	289	3	US-09-244-796-17
16	38	8.1	7898	4	US-08-984-709A-49
17	37	7.8	1413	4	US-08-171-389-392
18	35.6	7.5	50	1	US-08-123-936-392
19	35.6	7.5	50	2	US-08-475-228A-392
20	35.6	7.5	50	2	US-08-482-080A-392
21	35.6	7.5	50	3	US-09-354-947-392
22	35.6	7.5	50	3	PCT-US93-12388-392
23	35.6	7.5	50	5	US-09-027-064-3
24	34.2	7.2	1338	3	US-09-271-815-3
25	34.2	7.2	1338	3	US-09-027-064-1
26	34.2	7.2	2394	3	US-09-271-815-1
27	34.2	7.2	2394	3	US-09-271-815-1

28	34	7.2	1503	4	US-09-184-418C-29	Sequence 29, Appl
29	34	7.2	8953	4	US-09-184-418C-3	Sequence 3, Appl
30	33.8	7.2	2397	1	US-07-891-942G-11	Sequence 11, Appl
31	33.4	7.1	42325	4	US-08-311-731A-131	Sequence 131, Appl
32	33.2	7.0	248	3	US-09-007-005-32	Sequence 32, Appl
33	33.2	7.0	248	3	US-09-244-796-32	Sequence 32, Appl
34	33.2	7.0	277	3	US-09-007-005-3	Sequence 3, Appl
35	33.2	7.0	277	3	US-09-244-796-3	Sequence 3, Appl
36	32.6	6.9	3995	3	US-08-868-435-3	Sequence 3, Appl
37	32.6	6.9	3995	4	US-08-744-231-3	Sequence 3, Appl
38	32.2	6.8	164976	4	US-08-916-421B-1	Sequence 1, Appl
39	32	6.8	1298	3	US-08-948-705-3	Sequence 3, Appl
40	32	6.8	1298	4	US-09-510-543-3	Sequence 3, Appl
41	32	6.8	6755	3	US-08-931-999-4	Sequence 4, Appl
42	31.8	6.7	3383	1	US-07-707-367-1	Sequence 1, Appl
43	31.8	6.7	3989	4	US-09-205-258-28	Sequence 28, Appl
44	31.8	6.7	4117	4	US-09-484-970B-2	Sequence 2, Appl
45	31.6	6.7	486	4	US-09-510-252-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-033-556-7
; Sequence 7, Application US/09033556
; Patent No. 6432700
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
; TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
; TITLE OF INVENTION: OF USING SAME
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 100.0%; Score 472; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 6.3e-129;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for WI
; SEQ ID NO 10
; LENGTH: 15056
; TYPE: DNA
; ORGANISM: Homo Sapien
TS-09-474-699-10

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Query Match	1
Best Local	14062
Matches	61
	14122

QY	Db	14182	121
	QY	181	
	Db	14242	
QY	QY	241	
	Db	14302	
QY	QY	301	
	Db	14362	
QY	QY	361	
	Db	14422	
QY	QY	421	
	Db	14482	

RESULT 6
JUS-08-646-301A
Sequence 2, 6
Patent No. 6
GENERAL INFO:
APPLICANT:
APPLICANT:
TITLE OF INVENTION:
Patent No. 6
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION:
CURRENT FILING DATE:
NUMBER OF SEQUENCES:
SOFTWARE:
SEQ ID NO 2
LENGTH: 377
TYPE: DNA
ORGANISM: HOMO
JUS-08-646-301A

Query Match	4	1662
Best Local S	1	
Matches 185;		

RESULT 4	US-08-154-712B-4
Sequence 4	Applicant
Patent No.	6337
GENERAL INFORMATION	
APPLICANT:	Hull
APPLICANT:	Rice
TITLE OF INVENTION	
TITLE OF INVENTION	
FILE REFERENCE	
CURRENT APPLICANT	
CURRENT FILING	
NUMBER OF SEQ	
SOFTWARE:	Pat
SEQ ID NO 4	
LENGTH:	11288
TYPE:	DNA
ORGANISM:	Homo
US-08-154-712B-4	

Query Match	Best Local Similarity	Matches	471: C
Qy	1	AGCC	
Db	10294	AGCC	
Qy	61	GGCA	
Db	10354	GGCA	
Qy	121	TTTC	
Db	10414	TTTC	
Qy	181	CAGA	
Db	10474	CAGA	
Qy	241	GC GG	
Db	10534	GC GG	
Qy	301	GGCA	
Db	10594	GGCA	
Qy	361	CGTG	
Db	10654	CGTG	
Qy	421	GCAG	
Db	10714	GCAG	

RESULT 5
SS-09-474-699-10
Sequence 10, App
Patent No. 649511
GENERAL INFORMATION
APPLICANT: Henc
APPLICANT: Yu,
TITLE OF INVENT
TITLE OF INVENT
FILE REFERENCE:
CURRENT APPLIC
CURRENT FILING
PRIOR APPLICATI
PRIOR FILING DAT

QY 64 ATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGAGACCCCTGCTGGGTTT 123
Db 1722 ATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCCTGCTGGGTTT 1777
QY 124 CTCTGTCCACAAAGGAAATAATCCCTGGT-----GT 156
Db 1778 CTGCATCACAAGAAATAATCCCTGGT-----GT 1837
QY 157 GACAGACCCAGGAGACACAGACAGAGCTCAGCAGTGGGGAAGACAGGTTGCTCC 216
Db 1838 GACAGACCTGAGGACGAGATAGCAGAGCTAGCCCTAGGAGGTTGGTCCATCCACC 1897
QY 217 AGGGGATGGGGTCCATCCCTTGC 242
Db 1898 AGGGGACAGGGTGCACACGCTTGC 1923

RESULT 7
US-08-481-968A-5
; Sequence 5, Application US/08481968A
; Patent No. 6300490
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; APPLICANT: Richards, Cynthia
; TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (CEA)
; FILE OF INVENTION: Transcriptional Regulatory Region
; FILE REFERENCE: PB1087US4
; CURRENT APPLICATION NUMBER: US/08/481,968A
; CURRENT FILING DATE: 1998-06-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 3774
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-481-968A-5

Query Match 19.9%; Score 94; DB 4; Length 3774;
Best Local Similarity 69.5%; Pred. No. 6.7e-18;
Matches 185; Conservative 0; Mismatches 50; Indels 31; Gaps 3;
QY 4 CACACCCAGTGAGCCCTTTCTAGCCCCCAGAGCCCTCTGTACCTTCTGCTGGG 63
Db 1662 CAGTAAACAGTGAAGCTTCTATCCAGCCCCCAGAGCCCTCTGTACCTTCTGCTGGG 1721
QY 64 ATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGAGACCCCTGCTGGGTTT 123
Db 1722 ATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCCTGCTGGGTTT 1777
QY 124 CTCTGTCCACAAAGGAAATAATCCCTGGT-----GT 156
Db 1778 CTGCATCACAAGAAATAATCCCTGGT-----GT 1837
QY 157 GACAGACCCAGGAGACACAGACAGAGCTCAGCAGTGGGGAAGACAGGTTGCTCC 216
Db 1838 GACAGACCTGAGGACGAGATAGCAGAGCTAGCCCTAGGAGGTTGGTCCATCCACC 1897
QY 217 AGGGGATGGGGTCCATCCCTTGC 242
Db 1898 AGGGGACAGGGTGCACACGCTTGC 1923

RESULT 8
US-08-154-712B-5
; Sequence 5, Application US/08154712B
; Patent No. 637209
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; APPLICANT: Richards, Cynthia
; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen Regu
; FILE REFERENCE: PB1087US3

; CURRENT APPLICATION NUMBER: US/08/154,712B
; CURRENT FILING DATE: 1993-11-19
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 3774
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-154-712B-5
Query Match 19.9%; Score 94; DB 4; Length 3774;
Best Local Similarity 69.5%; Pred. No. 6.7e-18;
Matches 185; Conservative 0; Mismatches 50; Indels 31; Gaps 3;
QY 4 CACACCCAGTGAGCCCTTTCTAGCCCCCAGAGCCCTCTGTACCTTCTGCTGGG 63
Db 1662 CAGTAAACAGTGAAGCTTCTATCCAGCCCCCAGAGCCCTCTGTACCTTCTGCTGGG 1721
QY 64 ATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGAGACCCCTGCTGGGTTT 123
Db 1722 ATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCCTGCTGGGTTT 1777
QY 124 CTCTGTCCACAAAGGAAATAATCCCTGGT-----GT 156
Db 1778 CTGCATCACAAGAAATAATCCCTGGT-----GT 1837
QY 157 GACAGACCCAGGAGACACAGACAGAGCTCAGCAGTGGGGAAGACAGGTTGCTCC 216
Db 1838 GACAGACCTGAGGACGAGATAGCAGAGCTAGCCCTAGGAGGTTGGTCCATCCACC 1897
QY 217 AGGGGATGGGGTCCATCCCTTGC 242
Db 1898 AGGGGACAGGGTGCACACGCTTGC 1923
RESULT 9
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109

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; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
; US-08-232-463-14

Query Match      15.1%; Score 71.2; DB 1; Length 7218;
Best Local Similarity 4.0%; Pred. No. 4.1e-11;
Matches 16; Conservative 236; Mismatches 144; Indels 0; Gaps 0;

QY 76 TCCAGACCCCTGAGACATGGGAGACCGGACCGTGTGGTTCCTGTGCACAA 135
Db | | : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 136 GGAATAATCCCTGGTGACAGACCCCAAGGACACACACAGCAGTCACTG 195
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1377 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1318
QY 196 GGAAGACAGTTCCTCCAGGGGATGGGGTCCATCCACCTGCCGAAAGATTGT 255
Db | | : : : : : : : : : : : : : : : : : : : : : : : : : :
1317 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1258
QY 256 CTGAGGAACTGAAATAGACGGGAAAGAGAGGAGGACAAAGAGCAATGAGAG 315
Db | | : : : : : : : : : : : : : : : : : : : : : : : : : :
1257 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1198
QY 316 GGAGGGACAGAGACACCTGAATAAGACACACACACCATGACCCAGTGTGAGAAG 375
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QY 376 TACTCTGCCCTAGGAGAGACTCAGGCGAGGAGGAGGAGGACAGCAGCAGCAGTC 435
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QY 436 ACAGGACCTTGACAAACCTTCTGGAACCTCAGC 471
Db | | : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 10
US-09-370-838-177
; Sequence 177, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; FILE REFERENCE: 210121.475C1
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US/09/370,838
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 177
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-370-838-177

Query Match      12.2%; Score 57.6; DB 4; Length 387;
Best Local Similarity 93.8%; Pred. No. 1.2e-07;
Matches 60; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 408 GGGAGGAGGACAGCAGACGACGACGACGACGACGACGACGACGACGACG 467

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Db 7 GGCACACGAGCAGACGACGACGACGACGACGACGACGACGACGACGACGACG 66
QY 468 AAGC 471
Db 67 AAGC 70

RESULT 11
US-08-389-459A-16
; Sequence 16, Application US/08389459A
; Patent No. 5817512
; GENERAL INFORMATION:
; APPLICANT: Morrow, Casey D. and Porter, Donna, C.
; TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT POLIOVIRUS
; TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,459A
; FILING DATE: 15-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/087,009
; FILING DATE: 01-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: UAG-004CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2220 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2203
; US-08-389-459A-16

Query Match      11.4%; Score 54; DB 1; Length 2220;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 419 CAGCAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 472
Db 5 CAGCAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 58

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RESULT 12
US-08-987-867A-16
; Sequence 16, Application US/08987867A
; Patent No. 6063384
; GENERAL INFORMATION:
; APPLICANT: C. Morrow et al.
; TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL

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Copyright (c) 1993 - 2003 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
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(without alignments)
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Perfect score: 472
Sequence: 1 AGCCACACCCAGTGCCT.....ACGTTCTGCACTCAGCA 472
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1678620 seqs, 1244745471 residues
Total number of hits satisfying chosen parameters: 3357240
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	472	100.0	472	11	US-09-151-376-7
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3	472	100.0	472	12	US-10-139-089-7
4	472	100.0	472	12	US-10-139-089-7
5	472	100.0	472	14	US-10-045-116-1
6	471	99.8	11288	9	US-09-947-925A-4
7	471	99.8	11288	10	US-09-822-634-1
8	471	99.8	15056	9	US-09-392-822-4
9	471	99.8	15056	11	US-09-814-357-14
10	471	99.8	15056	12	US-09-814-351-14
11	471	99.8	15056	14	US-10-045-116-25
12	471	99.8	15056	14	US-10-226-820-10
13	432.4	91.6	3281	12	US-10-090-238-1
14	350.4	74.2	425	14	US-10-212-667-2
15	120.8	25.6	1855	13	US-10-027-632-97812
16	99.2	21.0	608	13	US-10-027-632-8715

17	94	19.9	3774	9	US-09-947-925A-5	Sequence 5, Appli
18	75	15.9	2974	10	US-09-954-456-56	Sequence 56, Appl
19	75	15.9	2974	10	US-09-880-107-2317	Sequence 2317, Ap
20	75	15.9	2974	14	US-10-157-031-340	Sequence 340, App
21	75	15.9	2974	14	US-10-207-655-86	Sequence 86, Appl
22	67.8	14.4	2547	12	US-09-814-353-20321	Sequence 20321, A
23	60.6	12.8	474	9	US-09-864-761-6512	Sequence 6512, Ap
24	59	12.5	1298	9	US-09-925-301-290	Sequence 290, App
25	57.6	12.2	387	10	US-09-738-973-177	Sequence 177, App
26	57.6	12.2	387	10	US-09-854-133-177	Sequence 177, App
27	57.6	12.2	387	14	US-10-144-649A-177	Sequence 177, App
28	57.2	12.1	460	9	US-09-922-217-169	Sequence 169, App
29	57.2	12.1	460	10	US-09-833-263-169	Sequence 169, App
30	57.2	12.1	460	13	US-10-025-380-169	Sequence 169, App
c 31	56	11.9	676	13	US-10-027-632-127633	Sequence 127633,
c 32	55.4	11.7	294	10	US-09-920-300A-311	Sequence 311, App
c 33	55.4	11.7	294	12	US-10-099-926-311	Sequence 311, App
c 34	55.4	11.7	294	13	US-10-033-528-311	Sequence 311, App
c 35	54	11.4	2220	9	US-09-756-551A-16	Sequence 16, Appl
c 36	52	11.0	288	9	US-09-815-343-1478	Sequence 1478, Ap
c 37	51.6	10.9	1833	12	US-09-814-353-20347	Sequence 20347, A
c 38	51.6	10.9	1833	14	US-10-198-846-13797	Sequence 13797, A
c 39	49.2	10.4	5975	12	US-10-311-455-210	Sequence 210, App
c 40	47	10.0	283	9	US-09-815-343-349	Sequence 349, App
c 41	44.2	9.4	319	11	US-09-871-161-486	Sequence 486, App
c 42	44.2	9.0	409	12	US-09-814-353-16466	Sequence 16466, A
c 43	42.4	9.0	627	14	US-10-198-846-7704	Sequence 7704, Ap
c 44	42.4	9.0	2134	14	US-10-208-408-5	Sequence 5, Appli
c 45	42.4	9.0	2364	14	US-10-198-846-10292	Sequence 10292, A

ALIGNMENTS

RESULT 1
US-09-151-376-7
; Sequence 7, Application US/09151376
; Publication No. US20030044383A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-151-376-7

Query Match	100.0%	Score 472;	DB 11;	Length 472;
Best Local Similarity	100.0%	Pred. No. 4.7e-137;		
Matches 472;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AGCCACACCCAGTGCAGCTTTTCTAGCCCCCAGAGCCACCTCTGTACCTTCCTGTTG	60	
Db	1	AGCCACACCCAGTGCAGCTTTTCTAGCCCCCAGAGCCACCTCTGTACCTTCCTGTTG	60	
QY	61	GCATCATCCACCTTCCAGAGCCCTGGAGAGATGGGAGACCCGGGACCCCTGCTGG	120	
Db	61	GCATCATCCACCTTCCAGAGCCCTGGAGAGATGGGAGACCCGGGACCCCTGCTGG	120	
QY	121	TTTCTCTCAAAAGGAAATAATCCCTGGTGTGACAGACCCAGGACAGACACAG	180	
Db	121	TTTCTCTCAAAAGGAAATAATCCCTGGTGTGACAGACCCAGGACAGACACAG	180	

QY 301 GCGAGAAATGAGAGGGGAGGACAGAGGACACCTGAATAAGAGACACACCCATGACCA 360
 Db 301 GCGAGAAATGAGAGGGGAGGACAGAGGACACCTGAATAAGAGACACACCCATGACCA 360
 QY 361 CGTGATGCTGAGAGTACTCTCGCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
 Db 361 CGTGATGCTGAGAGTACTCTCGCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
 QY 421 GCAGACAGACAGTCACAGAGCCTTGACAAAAAGTTCCTGGAACTCAAGCA 472
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RESULT 4

US-10-139-089-54
 ; Sequence 54, Application US/10139089
 ; Publication No. US20030152553A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Henderson, D.R.
 ; APPLICANT: Schuur, E.R.
 ; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
 ; FILE REFERENCE: 348022000221
 ; CURRENT APPLICATION NUMBER: US/10/139,089
 ; CURRENT FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: 08/669,753
 ; PRIOR FILING DATE: 1996-06-26
 ; PRIOR APPLICATION NUMBER: 08/495,034
 ; PRIOR FILING DATE: 1995-06-27
 ; PRIOR APPLICATION NUMBER: 09/509,591
 ; PRIOR FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: 09/151,376
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 09/033,428
 ; PRIOR FILING DATE: 1998-03-02
 ; PRIOR APPLICATION NUMBER: 60/039,597
 ; PRIOR FILING DATE: 1997-03-03
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 ; PRIOR FILING DATE: 1998-03-02
 ; PRIOR APPLICATION NUMBER: 60/039,763
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 ; PRIOR APPLICATION NUMBER: 09/033,333
 ; PRIOR FILING DATE: 1998-03-02
 ; PRIOR APPLICATION NUMBER: 60/039,762
 ; PRIOR FILING DATE: 1997-03-03
 ; NUMBER OF SEQ ID NOS: 71
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 54
 ; LENGTH: 472
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Unknown
 US-10-139-089-54

Query Match 100.0%; Score 472; DB 12; Length 472;
 Best Local Similarity 100.0%; Pred. No. 4.7e-137;
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGCCACCCAGCAGTGGAGCCTTTTCTAGCCCCAGAGCCACTCTGTCACTTCCTGTG 60
 Db 1 AGCCACCCAGCAGTGGAGCCTTTTCTAGCCCCAGAGCCACTCTGTCACTTCCTGTG 60
 QY 61 GGCATATCCACCTTCCAGAGCCTTGAGAGCATGGGAGACCCCGGACCCCTGCTGG 120
 Db 61 GGCATATCCACCTTCCAGAGCCTTGAGAGCATGGGAGACCCCGGACCCCTGCTGG 120
 QY 121 TTTCTCTGTCACAAAGGAAATAATCCCTGGTGTGACAGACCCCAAGGACAGACACAG 180
 Db 121 TTTCTCTGTCACAAAGGAAATAATCCCTGGTGTGACAGACCCCAAGGACAGACACAG 180
 QY 181 CAGAGGTGACGACATGGGAGACAGAGTTGCTCCAGGGATGGGGTCCATCCACCT 240
 Db 181 CAGAGGTGACGACATGGGAGACAGAGTTGCTCCAGGGATGGGGTCCATCCACCT 240

QY 241 GCGAGAAATGATTTGTCTGAGGAACCTGAAATAGAGGGAAAAAAGAGAGGACAAAGA 300
 Db 241 GCGAGAAATGATTTGTCTGAGGAACCTGAAATAGAGGGAAAAAAGAGAGGACAAAGA 300
 QY 301 GCGAGAAATGAGAGGGGAGGACAGAGGACACCTTGAAATAAGAGACACACCCATGACCA 360
 Db 301 GCGAGAAATGAGAGGGGAGGACAGAGGACACCTTGAAATAAGAGACACACCCATGACCA 360
 QY 361 CGTGATGCTGAGAGTACTCTCGCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
 Db 361 CGTGATGCTGAGAGTACTCTCGCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
 QY 421 GCAGACAGACAGTCACAGAGCCTTGACAAAAAGTTCCTGGAACTCAAGCA 472
 Db 421 GCAGACAGACAGTCACAGAGCCTTGACAAAAAGTTCCTGGAACTCAAGCA 472

RESULT 5

US-10-045-116-1
 ; Sequence 1, Application US/10045116
 ; Publication No. US20030026792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lamparski, Henry
 ; Schuur, Eric
 ; Henderson, Daniel
 ; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
 ; EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
 ; THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 PAGE MILL ROAD
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/10/045,116
 ; FILING DATE: 23-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; ADDITIONAL ADDRESS: US/09/000,555A
 ; FILING DATE: 02-Mar-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: POLIZZI, CATHERINE M.
 ; REGISTRATION NUMBER: 40,130
 ; REFERENCE/DOCKET NUMBER: 34802-30005.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141 MRSNFOERS SFO
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 472 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-045-116-1

Query Match 100.0%; Score 472; DB 14; Length 472;
 Best Local Similarity 100.0%; Pred. No. 4.7e-137;
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGCCACCCAGCAGTGGAGCCTTTTCTAGCCCCAGAGCCACTCTGTCACTTCCTGTG 60
 Db 1 AGCCACCCAGCAGTGGAGCCTTTTCTAGCCCCAGAGCCACTCTGTCACTTCCTGTG 60

QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGACCCCTGCTGGG 120
 Db 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGACCCCTGCTGGG 120
 QY 121 TTTCTCTGTCAAAAGGAAATATATCCCTTGGTGTGACAGACCCCAAGGAGACACAG 180
 Db 121 TTTCTCTGTCAAAAGGAAATATATCCCTTGGTGTGACAGACCCCAAGGAGACACAG 180
 QY 181 CAGAGGTGAGCACTGGGAGACAGGTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
 Db 181 CAGAGGTGAGCACTGGGAGACAGGTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
 QY 241 GCGGAAAGATTTGCTGAGGAACTGAAAATAGAGGGGAAAAAAGAGGGGACAAAAAGA 300
 Db 241 GCGGAAAGATTTGCTGAGGAACTGAAAATAGAGGGGAAAAAAGAGGGGACAAAAAGA 300
 QY 301 GGCAGAAATAGAGGGGAGGGGACAGAGACACCTGAAATAAGACACACCCATGACCCA 360
 Db 301 GGCAGAAATAGAGGGGAGGGGACAGAGACACCTGAAATAAGACACACCCATGACCCA 360
 QY 361 CGTGATGCTGAGAACTCTCCCTAGGAGAGACTCAGGCGAGAGGAGGAGGAGGACA 420
 Db 361 CGTGATGCTGAGAACTCTCCCTAGGAGAGACTCAGGCGAGAGGAGGAGGAGGACA 420
 QY 421 CGAGACACAGACTCAGAGCCCTTGACAAAAACGTTCTTGGAACTCAAGC 472
 Db 421 CGAGACACAGACTCAGAGCCCTTGACAAAAACGTTCTTGGAACTCAAGC 472

RESULT 6
 US-09-947-925A-4
 ; Sequence 4, Application US/09947925A
 ; Patent No. US20020055482A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Huber, Brian
 ; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic
 ; TITLE OF INVENTION: Antigen Regulatory
 ; TITLE OF INVENTION: Sequence
 ; FILE REFERENCE: PBI087U53
 ; CURRENT FILING DATE: 2001-09-06
 ; PRIOR APPLICATION NUMBER: US/09/947,925A
 ; PRIOR FILING DATE: 1993-11-19
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 11288
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: CDS
 ; LOCATION: (10804)....(10935)
 ; US-09-947-925A-4

Query Match 99.8%; Score 471; DB 9; Length 11288;
 Best Local Similarity 100.0%; Pred. No. 2.7e-136;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACTCTGTCACTTCTCTGTTG 60
 Db 10294 AGCCACACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACTCTGTCACTTCTCTGTTG 60
 QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGACCCCTGCTGGG 120
 Db 10354 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGACCCCTGCTGGG 120
 QY 121 TTTCTCTGTCAAAAGGAAATATATCCCTTGGTGTGACAGACCCCAAGGAGACACAG 180
 Db 10414 TTTCTCTGTCAAAAGGAAATATATCCCTTGGTGTGACAGACCCCAAGGAGACACAG 180
 QY 181 CAGAGGTGAGCACTGGGAGACAGGTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
 Db 10474 CAGAGGTGAGCACTGGGAGACAGGTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
 QY 241 GCGGAAAGATTTGCTGAGGAACTGAAAATAGAGGGGAAAAAAGAGGGGACAAAAAGA 300
 Db 10534 GCGGAAAGATTTGCTGAGGAACTGAAAATAGAGGGGAAAAAAGAGGGGACAAAAAGA 300
 QY 301 GGCAGAAATAGAGGGGAGGGGACAGAGACACCTGAAATAAGACACACCCATGACCCA 360
 Db 10594 GGCAGAAATAGAGGGGAGGGGACAGAGACACCTGAAATAAGACACACCCATGACCCA 360
 QY 361 CGTGATGCTGAGAACTCTCCCTAGGAGAGACTCAGGCGAGAGGAGGAGGAGGACA 420
 Db 10714 CGTGATGCTGAGAACTCTCCCTAGGAGAGACTCAGGCGAGAGGAGGAGGAGGACA 420

QY 241 GCGGAAAGATTTGCTGAGGAACTGAAAATAGAGGGGAAAAAAGAGGGGACAAAAAGA 300
 Db 10534 GCGGAAAGATTTGCTGAGGAACTGAAAATAGAGGGGAAAAAAGAGGGGACAAAAAGA 300
 QY 301 GGCAGAAATAGAGGGGAGGGGACAGAGGACACCTGAAATAAGACACACCCATGACCCA 360
 Db 10594 GGCAGAAATAGAGGGGAGGGGACAGAGGACACCTGAAATAAGACACACCCATGACCCA 360
 QY 361 CGTGATGCTGAGAACTCTCCCTAGGAGAGACTCAGGCGAGAGGAGGAGGAGGACA 420
 Db 10654 CGTGATGCTGAGAACTCTCCCTAGGAGAGACTCAGGCGAGAGGAGGAGGAGGACA 420
 QY 421 CGAGACACAGACTCAGAGCCCTTGACAAAAACGTTCTTGGAACTCAAGC 471
 Db 10714 CGAGACACAGACTCAGAGCCCTTGACAAAAACGTTCTTGGAACTCAAGC 471

RESULT 7
 US-09-822-634-1
 ; Sequence 1, Application US/09822634
 ; Patent No. US20020150556A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vile, Richard G.
 ; APPLICANT: Harrington, Kevin
 ; APPLICANT: Bateman, Andrew
 ; APPLICANT: Murphy, Steven
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
 ; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
 ; FILE REFERENCE: 07039-289001
 ; CURRENT APPLICATION NUMBER: US/09/822,634
 ; CURRENT FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: 60/193,977
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 11288
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (10804)....(10935)
 ; US-09-822-634-1

Query Match 99.8%; Score 471; DB 10; Length 11288;
 Best Local Similarity 100.0%; Pred. No. 2.7e-136;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACTCTGTCACTTCTCTGTTG 60
 Db 10294 AGCCACACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACTCTGTCACTTCTCTGTTG 60
 QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGACCCCTGCTGGG 120
 Db 10354 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGACCCCTGCTGGG 120
 QY 121 TTTCTCTGTCAAAAGGAAATATATCCCTTGGTGTGACAGACCCCAAGGAGACACAG 180
 Db 10414 TTTCTCTGTCAAAAGGAAATATATCCCTTGGTGTGACAGACCCCAAGGAGACACAG 180
 QY 181 CAGAGGTGAGCACTGGGAGACAGGTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
 Db 10474 CAGAGGTGAGCACTGGGAGACAGGTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
 QY 241 GCGGAAAGATTTGCTGAGGAACTGAAAATAGAGGGGAAAAAAGAGGGGACAAAAAGA 300
 Db 10534 GCGGAAAGATTTGCTGAGGAACTGAAAATAGAGGGGAAAAAAGAGGGGACAAAAAGA 300
 QY 301 GGCAGAAATAGAGGGGAGGGGACAGAGACACCTGAAATAAGACACACCCATGACCCA 360
 Db 10594 GGCAGAAATAGAGGGGAGGGGACAGAGACACCTGAAATAAGACACACCCATGACCCA 360
 QY 361 CGTGATGCTGAGAACTCTCCCTAGGAGAGACTCAGGCGAGAGGAGGAGGAGGACA 420
 Db 10714 CGTGATGCTGAGAACTCTCCCTAGGAGAGACTCAGGCGAGAGGAGGAGGAGGACA 420

; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15056
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-226-820-10

Query Match 99.8%; Score 471; DB 14; Length 15056;
Best Local Similarity 100.0%; Pred. No. 3e-136;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCACACCAGTGGAGCCCTTTTCTAGCCCCAGAGCCACCTCTGTACCTTCTCTGTTG 60
DB 14062 AGCCACACCAGTGGAGCCCTTTTCTAGCCCCAGAGCCACCTCTGTACCTTCTCTGTTG 14121
QY 61 GGATCATCCACCTTCCAGAGCCCTTGGAGAGCATGGGAGACCCCGGACCCCTGCTGGG 120
DB 14122 GGATCATCCACCTTCCAGAGCCCTTGGAGAGCATGGGAGACCCCGGACCCCTGCTGGG 14181
QY 121 TTTCTCTGTGTCACAAAGGAAATATCCCTTGGTGTGACAGACCCCAAGGACAGACAG 180
DB 14182 TTTCTCTGTGTCACAAAGGAAATATCCCTTGGTGTGACAGACCCCAAGGACAGACAG 14241
QY 181 CAGAGTTCAGCACTGGGGAAGACAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
DB 14242 CAGAGTTCAGCACTGGGGAAGACAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTT 14301
QY 241 GCCGAAAGATTTGTCTGAGAACTGAAATAGAGGAAAGGAGGAGGACAAAGA 300
DB 14302 GCCGAAAGATTTGTCTGAGAACTGAAATAGAGGAAAGGAGGAGGACAAAGA 14361
QY 301 GGAGAAATGAGAGGGGAGGAGGACAGAGACACCTGAATAGACACACCCATGACCCA 360
DB 14362 GGAGAAATGAGAGGGGAGGAGGACAGAGACACCTGAATAGACACACCCATGACCCA 14421
QY 361 CCGTATGCTGAGAACTACTCTCCCTAGGAGAGACTCAGGAGAGCTCAGGAGGAGGAGGAG 420
DB 14422 CCGTATGCTGAGAACTACTCTCCCTAGGAGAGACTCAGGAGAGCTCAGGAGGAGGAGGAG 14481
QY 421 GCAGACACAGCTACAGAGCCCTTGACAAACGTTCTCTGGAACCTCAAGC 471
DB 14482 GCAGACACAGCTACAGAGCCCTTGACAAACGTTCTCTGGAACCTCAAGC 14532

RESULT 13

US-10-090-238-1
; Sequence 1, Application US/10090238
; Publication No. US20030176377A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Rong Xiang
; APPLICANT: Ralph A. Reisfeld
; TITLE OF INVENTION: DNA VACCINES ENCODING CEA AND A CD40
; FILE REFERENCE: TSRT-830.0
; CURRENT APPLICATION NUMBER: US/10/090,238
; CURRENT FILING DATE: 2002-03-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3281
; TYPE: DNA
; ORGANISM: human
US-10-090-238-1

Query Match 91.6%; Score 432.4; DB 12; Length 3281;
Best Local Similarity 98.9%; Pred. No. 2e-124;
Matches 467; Conservative 0; Mismatches 1; Indels 4; Gaps 3;
QY 1 AGCCACACCAGTGGAGCCCTTTTCTAGCCCCAGAGCCACCTCTGTGACCTTCTCTGTTG 60
|||||

DB 1261 AGCCACACCAGTGGAGCCCTTTTCTAGCCCCAGAGCCACCTCTGTGACCTTCTCTGTTG 1320
QY 61 GGATCATCCACCTTCCAGAGCCCTTGGAGAGCATGGGAGACCCCGGACCCCTGCTGGG 120
DB 1321 GGATCATCCACCTTCCAGAGCCCTTGGAGAGCATGGGAGACCCCGGAG-CCTGCTGGG 1379
QY 121 TTTCTCTGTGTCACAAAGGAAATATCCCTTGGTGTGACAGACCCCAAGGACAGACACAG 180
DB 1380 TTTCTCTGTGTCACAAAGGAAATATCCCTTGGTGTGACAGACCCCAAGGACAGACACAG 1439
QY 181 CAGAGTTCAGCACTGGGG--AAGACAGGTTTCTCCAGGGGATGGGGTCCATCCACCT 239
DB 1440 CAGAGTTCAGCACTGGGGAAAGACAGGTTGTC--CAGAGGGATGGGGTCCATCCACCT 1497
QY 240 TCCGAAAGATTTGTCTGAGAACTGAATAGAGGAAAGGAGGAGGAGGAGGAGGAGGAG 299
DB 1498 TCCGAAAGATTTGTCTGAGAACTGAATAGAGGAAAGGAGGAGGAGGAGGAGGAGGAG 1557
QY 300 AGGAGAAATGAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 359
DB 1558 AGGAGAAATGAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1617
QY 360 ACCTGATGCTCAGAACTACTCTCCCTAGGAGAGACTCAGGAGGAGGAGGAGGAGGAGGAG 419
DB 1618 ACCTGATGCTCAGAACTACTCTCCCTAGGAGAGACTCAGGAGGAGGAGGAGGAGGAGGAG 1677
QY 420 AGCAGACACAGCTACAGCAGCCTTGACAAACGTTCTCTGGAACCTCAAGC 471
DB 1678 AGCAGACACAGCTACAGCAGCCTTGACAAACGTTCTCTGGAACCTCAAGC 1729

RESULT 14

US-10-212-667-2
; Sequence 2, Application US/10212667
; Publication No. US20030082722A1
; GENERAL INFORMATION:
; APPLICANT: FANG, BIANLIANG
; TITLE OF INVENTION: METHOD FOR AMPLIFYING EXPRESSION FROM A CELL SPECIFIC
; FILE REFERENCE: PROMOTER
; FILE REFERENCE: UTSC-708US
; CURRENT APPLICATION NUMBER: US/10/212,667
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/310,905
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-212-667-2

Query Match 74.2%; Score 350.4; DB 14; Length 425;
Best Local Similarity 98.7%; Pred. No. 3.7e-99;
Matches 385; Conservative 0; Mismatches 1; Indels 4; Gaps 3;
QY 83 GCCCTGGAGAGCATGGGAGACCCCGGACCCCTGCTGGGTTCTCTGTCAAAAGGAAAT 142
DB 1 GCCCTGGAGAGCATGGGAGACCCCGGAG-CCTGCTGGGTTCTCTGTCAAAAGGAAAT 59
QY 143 AATCCCTCTGGTGTGACAGACCCCAAGGACAGACAGAGGAGGAGGAGGAGGAGGAGGAG 201
DB 60 AATCCCTCTGGTGTGACAGACCCCAAGGACAGACAGAGGAGGAGGAGGAGGAGGAGGAG 119
QY 202 ACAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTTGTCCGAAAGATTTGCTGAGG 261
DB 120 ACAGGTTGTC--CAGAGGGGATGGGGTCCATCCACCTTGTCCGAAAGATTTGCTGAGG 177
QY 262 AACTGAAATAGAGGGGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 321
|||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 12:16:11 ; Search time 2041 Seconds
 (without alignments)
 5620.633 Million cell updates/sec

Title: US-10-045-116-1
 Perfect score: 472
 Sequence: 1 AGCCACCAACGAGCCT.....ACGTTCTGGAAGCA 472

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

EST:*

1: em_estba:.*
 2: em_esthum:.*
 3: em_estin:.*
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 6: em_estpl:.*
 7: em_estro:.*
 8: em_hic:.*
 9: gb_estl:.*
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 12: gb_est3:.*
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 16: em_estom:.*
 17: em_gss_hum:.*
 18: em_gss_inv:.*
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 20: em_gss_vrt:.*
 21: em_gss_fun:.*
 22: em_gss_mam:.*
 23: em_gss_mus:.*
 24: em_gss_pro:.*
 25: em_gss_rod:.*
 26: em_gss_phg:.*
 27: em_gss_vrl:.*
 28: gb_gssl:.*
 29: gb_gss2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87.8	18.6	328	9	AW449279
2	75.2	15.9	522	28	AZ553789
3	71	15.0	588	28	AZ377232
4	69	14.6	595	9	AL602851

5	68.8	14.6	787	9	AW140869
6	67	14.2	220	12	BM829043
7	67	14.2	275	12	BM836430
8	67	14.2	275	12	BM836430
9	67	14.2	355	12	BM752482
10	67	14.2	355	12	BM836104
11	67	14.2	418	12	BM751932
12	67	14.2	483	12	BM828560
13	67	14.2	569	12	BM836866
14	64.6	13.7	534	12	BM836866
15	63	13.3	879	28	AW746357
16	62	13.1	195	9	AW839587
17	61	12.9	651	9	AL602396
18	59	12.5	390	9	AA132598
19	57.4	12.2	574	2	HSW089849
20	56	11.9	887	12	BI759915
21	55	11.7	380	9	AA132182
22	53	11.2	997	29	CNS0005TE
23	52	11.0	506	13	BO561499
24	52	11.0	532	12	BM836657
25	52	11.0	639	12	BM236450
26	51.6	10.9	736	9	AL702861
27	50	10.6	300	9	AU099952
28	50	10.6	50	9	AU105569
29	50	10.6	835	14	CB995910
30	50	10.6	930	14	CB989395
31	50	10.6	1101	29	CNS0172T
32	49.8	10.6	1155	13	EX444199
33	49.8	10.6	882	13	EX445657
34	49.2	10.4	985	13	EX359916
35	49	10.4	691	2	HSM059861
36	49	10.4	523	2	HSM069649
37	48.8	10.3	1020	10	BG753754
38	48.8	10.3	595	2	HSW068872
39	48.4	10.3	772	14	CB994751
40	48.4	10.3	784	10	BG623391
41	48.4	10.3	821	14	CB997421
42	48.4	10.3	843	14	CB997034
43	48.4	10.3	847	14	CB989458
44	48.4	10.3	871	14	CB991637
45	48.4	10.3	989	14	CB995365

ALIGNMENTS

RESULT 1

AW449279

LOCUS

DEFINITION

AW449279 UI-H-BI3-akh-e-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone
 IMAGE:2734193 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW449279 328 bp mRNA linear EST 17-FEB-2000
 UI-H-BI3-akh-e-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone
 IMAGE:2734193 3', mRNA sequence.

AW449279.1 GI:6990055
 EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 328)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. cDNA Library preparation: M.B. Soares Lab Clone distribution:

NCI-CGAP clone distribution information: I.M.A.G.E. Consortium/INL at:

[www-bio.lnl.gov/bbrp/image.html](http://www.bio.lnl.gov/bbrp/image.html)

Seq primer: M13 Forward

AW140869 AU140869
 BM29043 K-EST0101
 BM836430 K-EST0112
 BM752482 K-EST0029
 BM836104 K-EST0111
 BM751932 K-EST0028
 BM828560 K-EST0101
 BM836866 K-EST0112
 BM752131 K-EST0028
 AW746357 HS-2278.A
 AW839587 RC6-LT007
 AL602396 DKFP686F
 AA132598 zol1c08.r
 BX779959 Homo sapi
 BI759915 603044336
 AA132182 z028b09.r
 AL60767 Drosophil
 BO561499 H4070F10-
 BM836657 K-EST0112
 BM236450 K0435E12-
 AL702861 DKFP686B
 AU099952 AU099952
 AU105569 AU105569
 CB995910 AGENCOURT
 CB989395 AGENCOURT
 AL107519 Drosophil
 EX444199 BX444199
 EX445657 BX445657
 EX359916 BX359916
 BX79971 Homo sapi
 BX479759 Homo sapi
 BG753754 602732559
 BX479086 Homo sapi
 CB994751 AGENCOURT
 CB961513 AGENCOURT
 BG623391 602648437
 CB997421 AGENCOURT
 CB997034 AGENCOURT
 CB989458 AGENCOURT
 CB991637 AGENCOURT
 CB995365 AGENCOURT

[illegible]

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Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 AGAGGGAGGAGGACAGACAGACAGACAGTTCACAGACGCTTGACAAAACGTTCTCGAA 464
Db 1 AGAGGGAGGAGGAGGACAGACAGACAGACAGTTCACAGACGCTTGACAAAACGTTCTCGAA 60
CTCAAGC 471
CTCAAGC 67

RESULT 7
BM836430 275 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0112089 S9SNU601 Homo sapiens cDNA clone S9SNU601-61-B06 5',
DEFINITION mRNA sequence.
ACCESSION BM836430
VERSION BM836430
KEYWORDS GI:19192839
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 275)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 61 row: B column: 06
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Location/Qualifiers
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Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dT primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with SfiI and
cloned into DraIII- digested pME18-FL3 vector. The
obtained cDNA vectors were used for transfection of
competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
BASE COUNT 71 a 90 c 67 g 47 t
ORIGIN

Query Match 14.2%; Score 67; DB 12; Length 275;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 AGAGGGAGGAGGACAGACAGACAGACAGTTCACAGACGCTTGACAAAACGTTCTCGAA 464
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CTCAAGC 471
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RESULT 8
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LOCUS K-EST0029023 S9SNU601 Homo sapiens cDNA clone S9SNU601-6-B10 5',
DEFINITION mRNA sequence.
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VERSION BM752482
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 279)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
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Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 6 row: B column: 10
High quality sequence stop: 279.
Location/Qualifiers
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Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
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cloned into DraIII- digested pME18-FL3 vector. The
obtained cDNA vectors were used for transfection of
competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
BASE COUNT 72 a 90 c 68 g 49 t
ORIGIN

Query Match 14.2%; Score 67; DB 12; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS K-EST0029023 S9SNU601 Homo sapiens cDNA clone S9SNU601-6-B10 5',
DEFINITION mRNA sequence.
ACCESSION BM752482
VERSION BM752482
KEYWORDS GI:19082100
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished
COMMENT Contact: Kim YS
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Korea Research Institute of Bioscience & Biotechnology
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 6 row: B column: 10
High quality sequence stop: 279.
Location/Qualifiers
1. 279
/organism="Homo sapiens"
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Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
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with tabacco acid pyrophosphatase (TAP). The decapped
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competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
BASE COUNT 72 a 90 c 68 g 49 t
ORIGIN

Query Match 14.2%; Score 67; DB 12; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 AGAGGGAGGAGGACAGACAGACAGACAGTTCACAGACGCTTGACAAAACGTTCTCGAA 464
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CTCAAGC 471
CTCAAGC 67

RESULT 10
BM752482 279 bp mRNA linear EST 04-MAR-2002
LOCUS K-EST0029023 S9SNU601 Homo sapiens cDNA clone S9SNU601-6-B10 5',
DEFINITION mRNA sequence.
ACCESSION BM752482
VERSION BM752482
KEYWORDS GI:19082100
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 279)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished
COMMENT Contact: Kim YS
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 6 row: B column: 10
High quality sequence stop: 279.
Location/Qualifiers
1. 279
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="S9SNU601"
/notes="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI;
Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
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site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dT primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with SfiI and
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competent cells E. coli Top10F, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
BASE COUNT 72 a 90 c 68 g 49 t
ORIGIN

Query Match 14.2%; Score 67; DB 12; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.00024;
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DEFINITION mRNA sequence.
ACCESSION BM752482
VERSION BM752482
KEYWORDS GI:19082100
SOURCE EST.
ORGANISM Homo sapiens (human
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VERSION
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REFERENCE
  1 (bases 1 to 355)
  Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
  Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
  Kim, Y.S.
TITLE
  21C Frontier Korean EST Project 2001
JOURNAL
  Unpublished
COMMENT
  Contact: Kim YS
  Genome Research Center
  Korea Research Institute of Bioscience & Biotechnology
  52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
  Tel: +82-42-860-4470
  Fax: +82-42-860-4409
  Email: yongsung@mail.kribb.re.kr
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      Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
      bacterial alkaline phosphatase (BAP) and then decapped
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      intact mRNA was ligated with DNA-RNA linker including Sfil
      site by treatment of T4 RNA ligase and the first strand
      cDNA was synthesized with Superscript II using Sfil
      oligo-dT primer. After first strand synthesis, RNA was
      degraded by NaOH treatment and cDNA was amplified by PCR
      reaction. The PCR products were digested with Sfil and
      cloned into DraIII- digested pME18S-FL3 vector. The
      obtained cDNA vectors were used for transformation of
      competent cells E. coli Top10F by electroporation method
      The cDNA libraries constructed by this method are
      full-length enriched cDNA library."
BASE COUNT
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Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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DB 1 AGGGGAGGAGGACAGACAGACAGAGTCCACAGCAGCCCTTGACAAAACGTTCTGGAA 60
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QY 465 CTAAGC 471
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SOURCE	Homo sapiens (human)
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REFERENCE	1 (bases 1 to 879)
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A.S., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
PUBMED	1049764
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 2278 row: A column: 8

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 195)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai M.A. da Silva, W. Jr., Zagó, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Balá, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F. de Souza, S.J. and

Search completed: September 26, 2003, 13:41:12
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